

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	11		ORF1475 polypeptide sequence SEQ ID NO:2950.		
1579	gi14327915	Homo sapiens	clone MGC:11186 IMAGE:3844322, mRNA, complete cds.	3446	100
1579	gi14043103	Homo sapiens	clone MGC:15388 IMAGE:3350378, mRNA, complete cds.	3446	100
1579	AAB94722	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15741.	3439	99
1580	gi13446190	Homo sapiens	Human DNA sequence from clone RP4-717M23 on chromosome 20 Contains the gene encoding a CRP2 binding protein (CRP2BP), a pseudogene, ESTs, STSs, GSSs and CpG islands, complete sequence.	3955	97
1580	gi14043103	Homo sapiens	clone MGC:15388 IMAGE:3350378, mRNA, complete cds.	3952	97
1580	gi14327915	Homo sapiens	clone MGC:11186 IMAGE:3844322, mRNA, complete cds.	3281	96
1581	gi16551610	Homo sapiens	cDNA FLJ31697 fis, clone NT2RI2005851, weakly similar to PLECTIN.	1911	99
1581	AAM66435	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 26741.	588	100
1581	AAM54044	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 26149.	588	100
1582	AAU20443	Homo sapiens	HUMA- Human secreted protein, Seq ID No 435.	940	94
1582	AAU93713	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3654.	756	100
1582	gi17149039	Homo sapiens	MT01-like protein gene, complete cds; nuclear gene for mitochondrial product.	756	100
1583	ABB12220	Homo sapiens	HYSE- Human peroxisomal Ca- dependent solute carrier homologue, SEQ:2590.	344	100
1583	gi12853685	Mus musculus	putative	168	52
1583	AAM80061	Homo sapiens	HYSE- Human protein SEQ ID NO 3707.	165	55
1584	gi14349125	Homo sapiens	mRNA for alpha2- glucosyltransferase (ALG10 gene).	716	93
1584	gi3513451	Rattus norvegicus	potassium channel regulator 1	681	90
1584	AAB25715	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 3 SEQ ID NO:104.	617	93
1585	gi12697939	Homo sapiens	mRNA for KIAA1697 protein, partial cds.	1904	100

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1585	gi10440249	Homo sapiens	cDNA: FLJ23529 fis, clone LNG06042.	1897	99
1585	gi7293415	Drosophila melanogaster	Dhc16F gene product	786	44
1586	AAZ35834_aal	Homo sapiens	INCY- Human vesicle trafficking protein 2 encoding cDNA.	804	84
1586	AAB93664	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13188.	804	84
1586	AAAY49959	Homo sapiens	INCY- Human vesicle trafficking protein 2.	804	84
1587	AAAY76561	Homo sapiens	META- Human ovarian tumor EST fragment encoded protein 57.	623	92
1587	gi13623585	Homo sapiens	Similar to RIKEN cDNA 1500034E06 gene, clone MGC:14151 IMAGE:3690202, mRNA, complete cds.	623	92
1587	gi12858676	Mus musculus	putative	595	88
1588	AAU20647	Homo sapiens	HUMA- Human secreted protein, Seq ID No 639.	927	99
1588	AAU20523	Homo sapiens	HUMA- Human secreted protein, Seq ID No 515.	927	99
1588	AAB95432	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17854.	927	99
1589	AAB59191	Homo sapiens	UYCO Human NADE.	293	57
1589	gi8452894	Homo sapiens	p75NTR-associated cell death executor (NADE) mRNA, complete cds.	293	57
1589	gi189379	Homo sapiens	Human unknown protein from clone pHGR74 mRNA, complete cds.	293	57
1590	AAG01716	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5797.	894	99
1590	AAAY82473	Homo sapiens	LLTL- Human APG12 protein sequence.	724	100
1590	gi4115731	Homo sapiens	mRNA for Apg12, complete cds.	724	100
1591	AAW87701	Homo sapiens	INCY- A human membrane fusion protein designated SYTAX1.	1357	99
1591	gi4200241	Homo sapiens	H.sapiens gene from PAC 42616, similar to syntaxin 7.	1325	100
1591	gi14715019	Mus musculus	Unknown (protein for MGC:6471)	1280	93
1592	AAA54089_aal	Homo sapiens	GETH PRO211 cDNA.	1944	87
1592	AAB53075	Homo sapiens	GETH Human angiogenesis-associated protein PRO211, SEQ ID NO:57.	1944	87
1592	AAB61231	Homo sapiens	MILL- Human TANGO 331 protein.	1944	87
1593	gi6681592	Homo sapiens	HSJ2 mRNA for DnaJ homolog, complete cds.	1567	93
1593	gi128032	Homo sapiens	MRJ gene for a member of the	1567	93

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	63		DNAJ protein family, clone MGC:1152 IMAGE:3346070, mRNA, complete cds.		
1593	AAW94066	Homo sapiens	INCY- Human DnaJ-like protein, HSPJ2.	1516	98
1594	gi11230858	Homo sapiens	mRNA for HMG-box transcription factor TCF-3, complete cds.	3096	100
1594	gi3123638	Mus musculus	TCF-3 protein	2934	95
1594	gi14279982	Xenopus laevis	T-cell factor XTcf-3	2195	77
1595	gi16307074	Homo sapiens	hypothetical protein FLJ22724, clone MGC:16791 IMAGE:3900548, mRNA, complete cds.	932	100
1595	gi10439225	Homo sapiens	cDNA: FLJ22724 fis, clone HSI14868.	932	100
1595	gi12854396	Mus musculus	putative	618	68
1596	gi10047229	Homo sapiens	mRNA for KIAA1577 protein, partial cds.	3874	100
1596	gi7959283	Homo sapiens	mRNA for KIAA1511 protein, partial cds.	3002	74
1596	gi10440418	Homo sapiens	mRNA for FLJ00044 protein, partial cds.	2010	63
1597	AAAY13117	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 131.	268	100
1597	gi13816407	Sulfolobus solfataricus	Dhydrogenase, putative	66	43
1597	gi15140082	Sinorhizobium meliloti	HYPOTHETICAL PROTEIN	66	37
1598	gi16943720	Homo sapiens	mRNA for SOX7 protein.	2106	100
1598	gi16550314	Homo sapiens	cDNA FLJ30994 fis, clone HLUNG1000076, highly similar to Mus musculus mRNA for mSox7.	2106	100
1598	gi13279164	Homo sapiens	Similar to SRY-box containing gene 7, clone MGC:10895 IMAGE:3622936, mRNA, complete cds.	2106	100
1599	gi17646146	Homo sapiens	B lymphocyte activation-related protein mRNA, complete cds.	1111	97
1599	gi12006223	Homo sapiens	NPD017 mRNA, complete cds.	1111	97
1599	gi15126745	Homo sapiens	hypothetical protein FLJ21174, clone MGC:5372 IMAGE:3445403, mRNA, complete cds.	1105	97
1600	gi14328879	Homo sapiens	CUB domain containing protein 1 (CDCP1) mRNA, complete cds.	4394	100
1600	gi10439515	Homo sapiens	cDNA: FLJ22969 fis, clone KAT10759.	4385	99
1600	AAAY914	Homo sapiens	HUMA- Human secreted protein	3633	98

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	56		sequence encoded by gene 6 SEQ ID NO:129.		
1601	gi12052846	Homo sapiens	mRNA; cDNA DKFZp564K2464 (from clone DKFZp564K2464); complete cds.	2152	100
1601	gi12652723	Homo sapiens	clone MGC:3295 IMAGE:3508204, mRNA, complete cds.	2035	100
1601	AAW79088	Homo sapiens	GEMY Human secreted protein bi129 2.	1115	100
1602	gi5081610	Mus musculus	huntington yeast partner C	4295	94
1602	gi15636898	Gallus gallus	formin binding protein 11- related protein	2507	55
1602	gi5081608	Mus musculus	formin binding protein 11	2505	54
1603	gi5081610	Mus musculus	huntington yeast partner C	4046	90
1603	gi6808038	Homo sapiens	mRNA; cDNA DKFZp434H2121 (from clone DKFZp434H2121); partial cds.	2341	100
1603	gi15636898	Gallus gallus	formin binding protein 11- related protein	2339	52
1604	AAB95053	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16855.	680	100
1604	gi10433525	Homo sapiens	cDNA FLJ12122 fis, clone MAMMA1000129.	680	100
1604	AAE06096	Homo sapiens	HUMA- Human gene 56 encoded secreted protein HRABA80, SEQ ID NO:158.	151	48
1605	AAB94309	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14777.	2318	99
1605	gi10434501	Homo sapiens	cDNA FLJ12800 fis, clone NT2RP2002079, weakly similar to HISTONE H1, GONADAL.	2318	99
1605	gi17391225	Mus musculus	Similar to hypothetical protein FLJ12800	1515	70
1606	AAG64502	Homo sapiens	UYFU- Human EPIP2 (endometrial progesterone- induced protein).	1914	100
1606	gi17390289	Homo sapiens	Similar to phosphoserine aminotransferase, clone MGC:9290 IMAGE:3883843, mRNA, complete cds.	1914	100
1606	gi13436074	Homo sapiens	Similar to phosphoserine aminotransferase, clone MGC:10519 IMAGE:3938160, mRNA, complete cds.	1914	100
1607	gi5326802	Homo sapiens	phosphoserine aminotransferase (PSA) mRNA, complete cds.	1673	100
1607	AAG64502	Homo sapiens	UYFU- Human EPIP2 (endometrial progesterone- induced protein).	1616	87
1607	gi17390289	Homo sapiens	Similar to phosphoserine aminotransferase, clone MGC:9290 IMAGE:3883843,	1616	87



SEQ ID	Hit ID	Species	Description	S score	Percent identity
			mRNA, complete cds.		
1608	gi13447761	Homo sapiens	cystatin and DUF19 domain-containing protein 1 (CSDUFL1) mRNA, complete cds.	736	100
1608	AAG74513	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5277.	570	100
1608	AAB93798	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13564.	281	47
1609	gi10440230	Homo sapiens	cDNA: FLJ23514 fis, clone LNG04628.	2005	100
1609	gi12852973	Mus musculus	putative	1509	69
1609	gi12407749	Arabidopsis thaliana	initiation factor 3a	138	22
1610	AAAY64994	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:1155.	372	100
1610	AAM00852	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 215.	69	39
1610	gi332565	Orf virus	ORF2	68	42
1611	gi10439705	Homo sapiens	cDNA: FLJ23121 fis, clone LNG07996.	3137	100
1611	AAB94996	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16625.	1618	99
1611	gi10433257	Homo sapiens	cDNA FLJ11889 fis, clone HEMBA1007251, weakly similar to Homo sapiens F-box protein FBX29 (FBX29) mRNA.	1618	99
1612	AAB95234	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17375.	3584	100
1612	gi10434674	Homo sapiens	cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mRNA.	3584	100
1612	gi5052031	Mus musculus	axotrophin	2983	85
1613	gi9650954	Mus musculus	beta-1,6-N-acetylglucosaminyltransferase B	1254	73
1613	AAV16000_aal	Homo sapiens	LJOL- Human beta-1,6-N-acetylglucosaminyltransferase (IGnT) encoding cDNA.	1044	65
1613	AAQ89201_aal	Homo sapiens	LJOL- I-branching enzyme cDNA.	1044	65
1614	gi10047311	Homo sapiens	mRNA for KIAA1617 protein, partial cds.	4792	100
1614	gi6635353	Homo sapiens	RUI (RUI) mRNA, complete cds.	2467	55
1614	gi15779095	Homo sapiens	Similar to RUI, clone MGC:3342 IMAGE:3029598, mRNA, complete cds.	2467	55
1615	gi4680693	Homo sapiens	CGI-27 protein mRNA, complete cds.	1414	92
1615	gi17511762	Homo sapiens	CGI-27 protein, clone MGC:31852 IMAGE:4851517, mRNA, complete cds.	1414	92
1615	gi170463	Homo sapiens	C21orf19-like protein mRNA,	1414	92

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	03		complete cds.		
1616	gi10047269	Homo sapiens	mRNA for KIAA1597 protein, partial cds.	4638	99
1616	gi13647069	Mus musculus	synaptotagmin-like protein 2-a delta 2S-III	3717	81
1616	gi13647009	Mus musculus	synaptotagmin-like protein 2-a	3666	77
1617	AAM93772	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3778.	1945	98
1617	ABB11731	Homo sapiens	HYSE- Human granuphilin-a homologue, SEQ ID NO:2101.	1945	98
1617	gi15930218	Homo sapiens	synaptotagmin-like 2, clone MGC:9588 IMAGE:3887570, mRNA, complete cds.	1945	98
1618	gi7768739	Homo sapiens	genomic DNA, chromosome 21q, section 89/105.	3747	100
1618	gi12857381	Mus musculus	putative	1233	78
1618	gi4884386	Homo sapiens	mRNA; cDNA DKFZp586F0422 (from clone DKFZp586F0422); partial cds.	870	80
1619	AAR22546	Homo sapiens	NEUR- Truncated Dopamine D1 receptor encoded by pseudogene clone GL-39.	1157	93
1619	AAR21082	Homo sapiens	NEUR- Dopamine D1 receptor encoded by clone GL-30.	1028	85
1619	gi32049	Homo sapiens	Human HD5DR gene for D5 dopamine receptor.	1028	85
1620	AAE10329	Homo sapiens	INCY- Human transporter and ion channel-6 (TRICH-6) protein.	1339	92
1620	AAM25877	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1392.	1284	100
1620	gi12856598	Mus musculus	putative	382	64
1621	AAB94278	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14707.	1465	100
1621	gi13543448	Homo sapiens	hypothetical protein FLJ12750, clone MGC:4691 IMAGE:3533384, mRNA, complete cds.	1465	100
1621	gi10434428	Homo sapiens	cDNA FLJ12750 fis, clone NT2RP2001168, weakly similar to VERPROLIN.	1465	100
1622	AAAY02669	Homo sapiens	HUMA- Human secreted protein encoded by gene 20 clone HMKAH10.	288	100
1622	gi7510421	Caenorhabditis elegans	hypothetical protein Y6G8.1 - Caenorhabditis elegans >	66	37
1623	AAB95393	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17745.	795	100
1623	gi10435217	Homo sapiens	cDNA FLJ13265 fis, clone OVARC1000937.	795	100
1623	AAB57019	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1597.	275	91
1624	AAG892	Homo sapiens	GEST Human secreted protein,	936	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	81		SEQ ID NO: 401.		
1624	AAU15932	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 885.	936	100
1624	gi10439193	Homo sapiens	cDNA: FLJ22700 fis, clone HSH12073.	936	100
1625	gi12857964	Mus musculus	putative	1533	86
1625	gi10241397	Homo sapiens	Human DNA sequence from clone RP3-336K20 on chromosome 6 Contains parts of 2 genes for novel proteins, ESTs, STSs and GSSs, complete sequence.	964	100
1625	gi16552303	Homo sapiens	cDNA FLJ32234 fis, clone PLACE6004687.	721	97
1626	gi10438158	Homo sapiens	cDNA: FLJ21940 fis, clone HEP04512.	3307	99
1626	AAG73712	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4476.	455	98
1626	gi10440614	Oryza sativa	putative ATP-dependent RNA helicase	452	32
1627	gi10437837	Homo sapiens	cDNA: FLJ21687 fis, clone COL09385.	1466	100
1627	gi6180178	Homo sapiens	transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha-1 subunit gene, partial cds, complete sequence.	1182	98
1627	ABB11561	Homo sapiens	HYSE- Human JM10 protein homologue, SEQ ID NO:1931.	947	100
1628	AAM25227	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:742.	2069	100
1628	AAB85362	Homo sapiens	INCY- Human phosphatase (PP) (clone ID 2522707CD1).	2021	100
1628	gi15080505	Homo sapiens	Similar to RIKEN cDNA 5730568A12 gene, clone MGC:17651 IMAGE:3857480, mRNA, complete cds.	1907	100
1629	gi6562845	Rattus norvegicus	type A/B hnRNP p40	1661	91
1629	gi3377279	Rattus norvegicus	AIF-C1	1654	91
1629	gi1814274	Homo sapiens	Human apobec-1 binding protein 1 mRNA, complete cds.	1631	92
1630	AAAY36083	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 468.	430	98
1630	AAG00583	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4664.	414	100
1630	gi358259	Cnemidophorus	NADH dehydrogenase subunit 4	66	37

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	4	tigris			
1631	AAB10284	Homo sapiens	GEMY Human fetal placenta protein fragment AC175_2i.	852	94
1631	gi3983463	Homo sapiens	microfibril-associated glycoprotein 2 (MAGP2) gene, exon 10 and complete cds.	852	94
1631	gi13543486	Homo sapiens	Microfibril-associated glycoprotein-2, clone MGC:14490 IMAGE:4247343, mRNA, complete cds.	852	94
1632	gi16198456	Homo sapiens	Similar to RIKEN cDNA 0610040E02 gene, clone MGC:17973 IMAGE:3919892, mRNA, complete cds.	1339	99
1632	AAAY02661	Homo sapiens	HUMA- Human secreted protein encoded by gene 12 clone HFTCU19.	1142	99
1632	gi16740689	Mus musculus	RIKEN cDNA 0610040E02 gene	1059	77
1633	AAB53094	Homo sapiens	GETH Human angiogenesis-associated protein PRO826, SEQ ID NO:158.	510	100
1633	AAB50916	Homo sapiens	GETH Human PRO826 protein.	510	100
1633	AAB65204	Homo sapiens	GETH Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.	510	100
1634	AAB53094	Homo sapiens	GETH Human angiogenesis-associated protein PRO826, SEQ ID NO:158.	413	85
1634	AAB50916	Homo sapiens	GETH Human PRO826 protein.	413	85
1634	AAB65204	Homo sapiens	GETH Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.	413	85
1635	gi10439008	Homo sapiens	cDNA: FLJ22573 fis, clone HSI02387.	1937	100
1635	AAM87876	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:15469.	187	45
1635	gi1334643	Xenopus laevis	APEG precursor protein	93	37
1636	gi10439008	Homo sapiens	cDNA: FLJ22573 fis, clone HSI02387.	578	100
1636	AAM87876	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:15469.	155	94
1636	gi3941365	Homo sapiens	I-REL gene, exon 12 and complete cds.	79	37
1637	AAM93871	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3980.	3761	99
1637	gi14331131	Homo sapiens	scinderin mRNA, complete cds.	3749	99
1637	AAR80481	Homo sapiens	NAKA/ Recombinant human adseverin.	3527	92
1638	gi10436970	Homo sapiens	cDNA: FLJ20991 fis, clone CAE02103.	239	67

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1638	gi6460240	Deinococcus radiodurans	DNA-binding response regulator	86	37
1638	gi16754877	Cyprinus carpio	Smad4 type4	79	27
1639	AAAY84901	Homo sapiens	INCY- A human proliferation and apoptosis related protein.	2821	95
1639	gi12053225	Homo sapiens	mRNA; cDNA DKFZp434P2235 (from clone DKFZp434P2235); complete cds.	2806	95
1639	gi37330	Homo sapiens	H.sapiens mRNA for tre oncogene (clone 210).	2053	78
1640	AAAY84901	Homo sapiens	INCY- A human proliferation and apoptosis related protein.	2846	96
1640	gi12053225	Homo sapiens	mRNA; cDNA DKFZp434P2235 (from clone DKFZp434P2235); complete cds.	2834	95
1640	gi37330	Homo sapiens	H.sapiens mRNA for tre oncogene (clone 210).	2050	77
1641	gi13936285	Mus musculus	TRH4	1522	77
1641	gi12845540	Mus musculus	putative	1520	77
1641	AAU00782	Homo sapiens	INCY- Human apoptosis protein, APOP-2.	1345	98
1642	gi17225331	Homo sapiens	MY0876G05 protein (MY876) mRNA, complete cds.	1209	100
1642	gi12002042	Homo sapiens	brain my048 protein mRNA, complete cds.	1209	100
1642	gi17646146	Homo sapiens	B lymphocyte activation-related protein mRNA, complete cds.	911	78
1643	gi10437307	Homo sapiens	cDNA: FLJ21240 fis, clone COL01132.	2090	100
1643	AAB74730	Homo sapiens	INCY- Human membrane associated protein MEMAP-36.	856	42
1643	AAAY94906	Homo sapiens	GEMY Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	853	42
1644	AAAY14448	Homo sapiens	HUMA- Human secreted protein encoded by gene 38 clone HFGAH44.	316	100
1645	gi10334443	Homo sapiens	Human DNA sequence from clone RP11-291L22 on chromosome 10 Contains the 3' end of the HSD17B7 (hydroxysteroid (17-beta) dehydrogenase 7) gene, part of a gene similar to CDC10 (cell division cycle 10, S. cerevisiae, homolog), part of a novel gene, a novel pseudogene, STSS, GSSs and a CpG Island, complete sequence.	256	100
1645	gi560623	human, fetal lung, mRNA, 2314 nt]. [Homo	hCDC10=CDC10 homolog	236	72

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		sapiens			
1645	gi2864606	Mus musculus	CDC10	236	72
1646	AAB18969	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	1707	95
1646	AAB49504	Homo sapiens	HUMA- Clone HNTMH27.	1370	94
1646	gi16307593	Mus musculus	RIKEN cDNA 2210021G21 gene	1325	90
1647	gi10047231	Homo sapiens	mRNA for KIAA1578 protein, partial cds.	2083	95
1647	gi6841194	Homo sapiens	HSPC272	281	81
1647	gi10800375	Caenorhabditis elegans	Hypothetical protein Y67D8C.5	192	21
1648	gi14349355	Homo sapiens	hypothetical protein FLJ23323, clone MGC:14873 IMAGE:3948222, mRNA, complete cds.	1771	100
1648	gi10439969	Homo sapiens	cDNA: FLJ23323 fis, clone HEP12456.	1771	100
1648	gi12852502	Mus musculus	putative	1540	65
1649	AAAY41360	Homo sapiens	HUMA- Human secreted protein encoded by gene 53 clone HJPAD75.	490	100
1649	AAM24406	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1931.	335	100
1649	AAAY41470	Homo sapiens	HUMA- Fragment of human secreted protein encoded by gene 53.	84	100
1650	AAAY41360	Homo sapiens	HUMA- Human secreted protein encoded by gene 53 clone HJPAD75.	267	63
1650	AAM24406	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1931.	199	90
1650	AAAY41470	Homo sapiens	HUMA- Fragment of human secreted protein encoded by gene 53.	84	100
1651	gi16550312	Homo sapiens	cDNA FLJ30993 fis, clone HLUNG1000064, weakly similar to KARYOGAMY PROTEIN KAR4.	2449	100
1651	gi16306892	Homo sapiens	clone MGC:2902 IMAGE:3010654, mRNA, complete cds.	2449	100
1651	gi13938595	Homo sapiens	Similar to CG7818 gene product, clone MGC:4531 IMAGE:3010654, mRNA, complete cds.	2449	100
1652	AAG67158	Homo sapiens	MILL- Amino acid sequence of a human 20685 transporter polypeptide.	1586	100
1652	gi13274122	Homo sapiens	Human DNA sequence from clone RP1-55C23 on chromosome 6q22.3-23.3 Contains the VNN1 and VNN2	1586	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			genes for vanin 1 and 2, the gene for vanin 3 (VNN3), a HLF (hepatic leukemia factor) pseudogene, a CCNG1 (cyclin G1) pseudogene, the 3' part of a novel gene, ESTs, GSSs, and STSSs, complete sequence.		
1652	gil5795817	Homo sapiens	unnamed protein product	1586	100
1653	AAB54163	Homo sapiens	HUMA- Human pancreatic cancer antigen protein sequence SEQ ID NO:615.	322	63
1653	gil80886	Homo sapiens	Human colipase mRNA, complete cds.	322	63
1653	gil7389764	Homo sapiens	colipase, pancreatic, clone MGC:23801 IMAGE:4251084, mRNA, complete cds.	322	63
1654	AAU17198	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 763.	1359	100
1654	gil5987493	Homo sapiens	tumor endothelial marker 6 (TEM6) mRNA, complete cds.	1359	100
1654	gil4325770	Homo sapiens	mRNA for thyroid specific PTB domain protein, complete cds.	1359	100
1655	AAG01118	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5199.	360	100
1655	gil5418966	Xenopus laevis	annexin 4	66	44
1656	gil0437031	Homo sapiens	cDNA: FLJ21034 fis, clone CAE09073.	1403	100
1656	gil6307159	Mus musculus	Unknown (protein for IMAGE:3493084)	1060	50
1656	gil13879551	Mus musculus	Unknown (protein for IMAGE:3709003)	1060	50
1657	AAM80047	Homo sapiens	HYSE- Human protein SEQ ID NO 3693.	820	91
1657	AAM79063	Homo sapiens	HYSE- Human protein SEQ ID NO 1725.	820	89
1657	ABB12144	Homo sapiens	HYSE- Human HSPP-29 protein homologue, SEQ ID NO:2514.	820	91
1658	gi5813823	Homo sapiens	SUI1 isolog mRNA, complete cds.	470	86
1658	gi450281	Homo sapiens	sui1 iso1 mRNA, complete cds.	470	86
1658	gi14250520	Homo sapiens	putative translation initiation factor, clone MGC:15684 IMAGE:3350981, mRNA, complete cds.	470	86
1659	gil6877187	Homo sapiens	clone MGC:17299 IMAGE:3845811, mRNA, complete cds.	1094	100
1659	AAV12952	Homo sapiens	HUMA- Amino acid sequence of a human secreted peptide.	362	98
1659	gi2394376	Cercopithecus aethiops	thromboxane A2 receptor; TBXA2R	94	29
1660	gi10438946	Homo sapiens	cDNA: FLJ22527 fis, clone HIRC12820.	1017	97
1660	gi165493	Homo sapiens	cDNA FLJ30149 fis, clone	665	90

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	12		BRACE2000280, weakly similar to MNN4 PROTEIN.		
1660	gi7299207	Drosophila melanogaster	CG16789 gene product	519	42
1661	AAB95572	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18221.	2231	100
1661	gi10435927	Homo sapiens	cDNA FLJ13798 fis, clone THYRO1000124.	2231	100
1661	gi12851620	Mus musculus	putative	1745	77
1662	AAY48256	Homo sapiens	META- Human prostate cancer-associated protein 42.	242	75
1662	gi3820857	Euglena spirogyra	maturase-like protein	81	30
1662	gi11559649	Leuconostoc mesenteroides	dextranucrase Dsrb742	79	39
1663	gi14017783	Homo sapiens	mRNA for KIAA1783 protein, partial cds.	2287	100
1663	AAU17193	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 758.	1725	100
1663	AAV57895	Homo sapiens	INCY- Human transmembrane protein HTMPN-19.	1634	100
1664	gi10436992	Homo sapiens	cDNA: FLJ21007 fis, clone CAE03871.	3436	100
1664	gi13784943	Mus musculus	Unknown (protein for MGC:11761)	2930	84
1664	gi17862868	Drosophila melanogaster	RE01471p	308	28
1665	AAG93318	Homo sapiens	NISC- Human protein HP10505.	465	100
1665	gi16306868	Homo sapiens	mitochondrial ribosomal protein S21, clone MGC:2680 IMAGE:2819715, mRNA, complete cds.	465	100
1665	gi13620911	Homo sapiens	MRPS21 mRNA for mitochondrial ribosomal protein S21, complete cds.	465	100
1666	AAU27652	Homo sapiens	ZYMO Human protein AFP213641.	1484	100
1666	gi15862470	Homo sapiens	unnamed protein product	1484	100
1666	AAE06071	Homo sapiens	HUMA- Human gene 31 encoded secreted protein HBJLF01, SEQ ID NO:133.	1284	100
1667	AAW78132	Homo sapiens	HUMA- Human secreted protein encoded by gene 7 clone HPEBD85.	246	100
1668	AAM50213	Homo sapiens	CURA- Human interleukin-11-like AMF7 C-terminal polypeptide.	2219	99
1668	gi16548921	Homo sapiens	unnamed protein product	2219	99
1668	AAB94803	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15937.	1358	100
1669	gi12053365	Homo sapiens	mRNA; cDNA DKFZp586O0222 (from clone	2747	100



SEQ ID	Hit ID	Species	Description	S score	Percent identity
			DKFZp586O0222); complete cds.		
1669	gi9368538	Homo sapiens	mRNA full length insert cDNA clone EUROIMAGE 1987170.	2687	98
1669	gi9965905	Mus musculus	synembryon	2383	86
1670	gi10440280	Homo sapiens	cDNA: FLJ23554 fis, clone LNG09359.	3757	100
1670	gi12855247	Mus musculus	putative	1339	64
1670	gi14602609	Homo sapiens	hypothetical protein FLJ23554, clone MGC:14866 IMAGE:3946091, mRNA, complete cds.	1236	99
1671	gi10441732	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds.	4286	99
1671	gi17382894	Homo sapiens	unnamed protein product	3899	93
1671	gi17382882	Mus musculus	unnamed protein product	3477	84
1672	AAB94118	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14362.	1936	100
1672	gi10434108	Homo sapiens	cDNA FLJ12552 fis, clone NT2RM4000712, moderately similar to Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA.	1936	100
1672	AAB95806	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18793.	1930	99
1673	AAB48293	Homo sapiens	UYVA Human ZF5 protein.	1407	80
1673	gi6456114	Mus musculus	F-box protein FBX16	1407	80
1673	ABBI5590	Homo sapiens	HUMA- Human nervous system related polypeptide SEQ ID NO 4247.	831	90
1674	gi10047163	Homo sapiens	mRNA for KIAA1549 protein, partial cds.	7563	100
1674	AAM79157	Homo sapiens	HYSE- Human protein SEQ ID NO 1819.	948	28
1674	AAM80141	Homo sapiens	HYSE- Human protein SEQ ID NO 3787.	941	30
1675	gi16768654	Drosophila melanogaster	HL01494p	911	39
1675	gi7292299	Drosophila melanogaster	CG1271 gene product	888	38
1675	gi4981995	Thermotoga maritima	glycerol kinase	846	38
1676	gi12852837	Mus musculus	putative	892	69
1676	gi3228237	Homo sapiens	UHS KerB gene.	871	71
1676	gi200962	Mus musculus	serine 1 ultra high sulfur protein	827	65
1677	gi17390182	Homo sapiens	clone IMAGE:4797244, mRNA, partial cds.	1694	99
1677	AAAY761	Homo sapiens	HUMA- Human secreted protein	863	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	77		encoded by gene 54.		
1677	AAAY04306	Homo sapiens	HUMA- Human secreted protein encoded by gene 14.	328	93
1678	gi5689417	Homo sapiens	mRNA for KIAA1040 protein, partial cds.	2793	99
1678	gi10728660	Drosophila melanogaster	CG8683 gene product	2736	48
1678	AAAY02367	Homo sapiens	ONOF Polypeptide identified by the signal sequence trap method.	2663	99
1679	gi10439964	Homo sapiens	cDNA: FLJ23320 fis, clone HEP12381.	3605	99
1679	AAG74499	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5263.	623	95
1679	gi12830679	Drosophila helvetica	putative transposase	220	24
1680	gi10438277	Homo sapiens	cDNA: FLJ22028 fis, clone HEP08589.	2454	100
1680	AAB73681	Homo sapiens	INCY- Human oxidoreductase protein ORP-14.	2337	100
1680	gi7298659	Drosophila melanogaster	CG10721 gene product	882	43
1681	AAB94393	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14957.	3231	99
1681	gi10434765	Homo sapiens	cDNA FLJ12973 fis, clone NT2RP2006023.	3231	99
1681	gi12860450	Mus musculus	putative	1177	64
1682	gi10437748	Homo sapiens	cDNA: FLJ21615 fis, clone COL07393.	876	100
1682	gi13195151	Homo sapiens	transcription factor T2P (T2P) mRNA, complete cds.	362	47
1682	gi10241461	Homo sapiens	Human DNA sequence from clone RP5-1121G12 on chromosome 20 Contains the 3' end of a gene encoding the hepatocellular carcinoma-associated antigen 58 (HCA58), the SCAND1 gene encoding the domain-containing 1 protein, a novel gene, 2 CpG islands, ESTs, STSs and GSSs, complete sequence.	362	47
1683	AAB43900	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1345.	483	87
1683	gi1684917	Homo sapiens	Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.	483	87
1683	gi12804705	Homo sapiens	ribosomal protein L44, clone MGC:2064 IMAGE:3353669, mRNA, complete cds.	483	87
1684	AAAY07931	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 80.	213	100
1684	gi593200	Mus musculus	neuronal apoptosis inhibitory	68	50

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	3		protein-rs6		
1684	gi5932008	Mus musculus	neuronal apoptosis inhibitory protein	68	50
1685	gi14030407	Mus musculus	keratin-associated protein 16.4	380	77
1685	gi14030409	Mus musculus	keratin-associated protein 16.5	309	64
1685	gi14030401	Mus musculus	keratin-associated protein 16.1	302	67
1686	gi15341794	Homo sapiens	hypothetical protein FLJ12787, clone MGC:16870 IMAGE:3048487, mRNA, complete cds.	1433	100
1686	AAB95182	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17250.	1426	99
1686	gi10434481	Homo sapiens	cDNA FLJ12787 fis, clone NT2RP2001943.	1426	99
1687	AAY38401	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 16.	230	88
1687	AAB25687	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 23 SEQ ID NO:76.	66	38
1688	gi12744921	Homo sapiens	tethering factor SEC34 (SEC34) mRNA, complete cds.	4223	100
1688	gi14549669	Homo sapiens	vesicle docking protein SEC34 mRNA, complete cds.	4212	99
1688	gi15291537	Drosophila melanogaster	GH25768p	1691	43
1689	AAB90746	Homo sapiens	GEMY Human DF989_3 protein sequence SEQ ID 192.	545	97
1689	AAW64471	Homo sapiens	GEMY Human secreted protein from clone DF989_3.	545	97
1689	gi2829302	Homo sapiens	mRNA for Efs1, complete cds.	74	37
1690	AAW13658	Homo sapiens	UYMC- Human cytidine deaminase.	657	87
1690	gi598149	Homo sapiens	cytidine deaminase (CDA) mRNA, complete cds.	657	87
1690	gi4321793	Homo sapiens	cytidine deaminase gene, exon 4 and complete cds.	657	87
1691	gi12698079	Homo sapiens	mRNA for KIAA1767 protein, partial cds.	4013	99
1691	AAM25578	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1093.	3955	99
1691	AAE06186	Homo sapiens	HUMA- Human gene 58 encoded secreted protein fragment, SEQ ID NO:248.	3521	99
1692	gi2559010	Homo sapiens	chaperonin containing t-complex polypeptide 1, eta subunit (Ccth) mRNA, complete cds.	890	100
1692	gi14198388	Mus musculus	chaperonin subunit 7 (eta)	879	98
1692	gi468504	Mus musculus	CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT)	879	98
1693	gi16552036	Homo sapiens	cDNA FLJ32028 fis, clone NTONG1000257.	918	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1693	AAB74768	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 13 SEQ ID NO:77.	592	99
1693	AAB74745	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 13 SEQ ID NO:54.	592	99
1694	gi10047157	Homo sapiens	mRNA for KIAA1546 protein, partial cds.	3652	100
1694	gi12697897	Homo sapiens	mRNA for KIAA1676 protein, partial cds.	613	39
1694	gi7292283	Drosophila melanogaster	CG2083 gene product	534	35
1695	AAG00078	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4159.	164	80
1695	gi2370202	Homo sapiens	mRNA for procollagen alpha 2(V).	164	80
1695	gi179698	Homo sapiens	Human collagen type V alpha-2 mRNA, 5' end.	164	80
1696	gi16552596	Homo sapiens	cDNA FLJ32466 fis, clone SKNMC2000065.	2609	99
1696	gi14017827	Homo sapiens	mRNA for KIAA1805 protein, partial cds.	2609	99
1696	gi15207987	Macaca fascicularis	hypothetical protein	2588	99
1697	AAB92879	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11475.	639	73
1697	AAM41435	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6366.	639	73
1697	AAM39649	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2794.	639	73
1698	AAM25487	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1002.	586	100
1698	AAG03667	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7748.	582	99
1698	gi12850050	Mus musculus	putative	557	93
1699	AAE04774	Homo sapiens	INCY- Human vesicle trafficking protein-17 (VETRP-17) protein.	748	100
1699	AAB41637	Homo sapiens	CURA- Human ORFX ORF1401 polypeptide sequence SEQ ID NO:2802.	748	100
1699	gi3319953	Homo sapiens	mRNA for TOM1 protein.	638	82
1700	gi14140100	Homo sapiens	OTT gene for one twenty two proteins (spliced and unspliced forms).	4797	99
1700	AAB95111	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17093.	4779	99
1700	gi14161369	Homo sapiens	putative RNA-binding motif protein 15 short form (RBM15) mRNA, complete cds, alternatively spliced.	4779	99
1701	AAB93879	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13792.	2228	100
1701	AAG66710	Homo sapiens	BIOD- Human cell growth inhibition protein 48.	2228	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1701	gi14495627	Homo sapiens	clone MGC:15047 IMAGE:3535485, mRNA, complete cds.	2228	100
1702	AAE11780	Homo sapiens	INCY- Human kinase (PKIN)-14 protein.	4186	100
1702	gi14041817	Homo sapiens	gklp mRNA for kinase-like protein splice variant 1, complete cds.	4186	100
1702	AAB65679	Homo sapiens	SUGE- Novel protein kinase, SEQ ID NO: 207.	4158	97
1703	AAU12253	Homo sapiens	GETH Human PRO5774 polypeptide sequence.	440	74
1703	AAV30734	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	258	96
1703	gi1181669	Saccharomyces cerevisiae	Tel2p	75	24
1704	gi10439762	Homo sapiens	cDNA: FLJ23164 fis, clone LNG09764.	3205	100
1704	gi10440312	Homo sapiens	cDNA: FLJ23577 fis, clone LNG12640.	1755	98
1704	gi12698085	Homo sapiens	mRNA for KIAA1770 protein, partial cds.	1614	99
1705	AAM41806	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6737.	1194	77
1705	AAM40020	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3165.	1194	77
1705	ABB12231	Homo sapiens	HYSE- Human novel protein, SEQ ID NO:2601.	1194	77
1706	gi15277565	Mus musculus	RIKEN cDNA 2510039O18 gene	3091	91
1706	gi12846932	Mus musculus	putative	3088	91
1706	AAB43028	Homo sapiens	CURA- Human ORFX ORF2792 polypeptide sequence SEQ ID NO:5584.	2246	95
1707	gi16041136	Macaca fascicularis	hypothetical protein	702	92
1707	AAB65216	Homo sapiens	GETH Human PRO1004 (UNQ488) protein sequence SEQ ID NO:227.	569	92
1707	AAV66693	Homo sapiens	GETH Membrane-bound protein PRO1004.	569	92
1708	AAB95636	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18369.	2429	100
1708	gi10436357	Homo sapiens	cDNA FLJ14009 fis, clone Y79AA1002431, weakly similar to TRANSDUCIN-LIKE ENHANCER PROTEIN 2.	2429	100
1708	gi5030439	Homo sapiens	chromosome 19, cosmid R26610, complete sequence.	1569	80
1709	gi15705143	Mus musculus	suppressor of cytokine signalling 4	2071	86
1709	AAM00759	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 122.	1712	100
1709	AAM00872	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 348.	1215	99
1710	gi104387	Homo sapiens	cDNA: FLJ22408 fis, clone	1934	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	85		HRC08416.		
1710	AAM39917	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3062.	837	45
1710	AAM41703	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6634.	836	45
1711	gi10437428	Homo sapiens	cDNA: FLJ21343 fis, clone COL02679.	1836	100
1711	gi12053145	Homo sapiens	mRNA; cDNA DKFZp434A0926 (from clone DKFZp434A0926); complete cds.	1388	99
1711	gi5689537	Homo sapiens	mRNA for KIAA1100 protein, complete cds.	1261	68
1712	AAG03254	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7335.	438	89
1712	gi7300383	Drosophila melanogaster	CG7671 gene product	366	27
1712	AAB94551	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15312.	309	100
1713	gi14495658	Homo sapiens	hypothetical protein FLJ12687, clone MGC:15791 IMAGE:3504468, mRNA, complete cds.	2639	99
1713	AAB94241	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14627.	2631	99
1713	gi10434333	Homo sapiens	cDNA FLJ12687 fis, clone NT2RM4002532, weakly similar to PROTEIN HOM1.	2631	99
1714	AAC62351_aa1	Homo sapiens	CELL- Nucleotide sequence of lysophosphatidic acid acyltransferase-beta.	834	100
1714	AAA39292_aa1	Homo sapiens	CELL- Human lysophosphatidic acid acyltransferase beta encoding cDNA.	834	100
1714	AAB30623	Homo sapiens	CELL- Amino acid sequence of lysophosphatidic acid acyltransferase-beta.	834	100
1715	AAB95847	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18896.	675	100
1715	gi10436763	Homo sapiens	cDNA FLJ14326 fis, clone PLACE4000247.	675	100
1715	gi16552900	Homo sapiens	cDNA FLJ32711 fis, clone TEST12000707, weakly similar to DOUBLESEX PROTEIN, MALE-SPECIFIC.	90	35
1716	AAB53094	Homo sapiens	GETH Human angiogenesis-associated protein PRO826, SEQ ID NO:158.	278	100
1716	AAB50916	Homo sapiens	GETH Human PRO826 protein.	278	100
1716	AAB65204	Homo sapiens	GETH Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.	278	100
1717	AAB94915	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16349.	961	100
1717	gi14602623	Homo sapiens	hypothetical protein FLJ11526, clone MGC:15059	961	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			IMAGE:3937610, mRNA, complete cds.		
1717	gi10432797	Homo sapiens	cDNA FLJ11626 fis, clone HEMBA1001655, weakly similar to Homo sapiens mSin3A associated polypeptide p30 mRNA.	961	100
1718	AAY12439	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:470.	453	94
1718	gi13477183	Homo sapiens	Similar to hypothetical protein FLJ20859, clone MGC:12940 IMAGE:2822127, mRNA, complete cds.	453	94
1718	gi12830810	Homo sapiens	false p73 target protein gene, complete cds.	453	94
1719	gi15928965	Homo sapiens	hypothetical protein FLJ11354, clone MGC:22961 IMAGE:4865798, mRNA, complete cds.	3522	100
1719	AAB93708	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13299.	3514	99
1719	gi10432595	Homo sapiens	cDNA FLJ11354 fis, clone HEMBA1000129, weakly similar to HYPOTHETICAL HELICASE C8A4.08C IN CHROMOSOME 1.	3514	99
1720	gi14717396	Homo sapiens	potassium-dependent Na/Ca exchanger NCKX3 (SLC24A3) mRNA, partial cds.	3108	97
1720	gi12597441	Mus musculus	K <sup>+</sup> -dependent Na/Ca exchanger	3027	94
1720	gi12000397	Rattus norvegicus	potassium-dependent sodium-calcium exchanger NCKX3	3025	94
1721	gi15072454	Mus musculus	von Willebrand factor A-related protein	1614	72
1721	AAB42581	Homo sapiens	CURA- Human ORFX ORF2345 polypeptide sequence SEQ ID NO:4690.	1358	93
1721	AAB88340	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0053.	1288	98
1722	AAB03822	Homo sapiens	HUMA- Human gene 5 encoded secreted protein HETKL27, SEQ ID NO: 68.	935	100
1722	AAB82597	Homo sapiens	HUMA- Human transmembrane protein encoded by cDNA clone HNALE36.	935	100
1722	gi15706437	Homo sapiens	clone MGC:17366 IMAGE:3860009, mRNA, complete cds.	935	100
1723	AAG66503	Homo sapiens	BIOD- Human ATP-dependent helicase 31.	1441	100
1723	AAM25780	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1295.	1441	100
1723	gi13676356	Homo sapiens	clone MGC:2679 IMAGE:2819663, mRNA, complete cds.	1434	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1724	AAG67394	Homo sapiens	SUGE- Amino acid sequence of human protein kinase SGK269.	2322	100
1724	gi10437181	Homo sapiens	cDNA: FLJ21140 fis, clone CAS07548.	1730	100
1724	AAG67393	Homo sapiens	SUGE- Amino acid sequence of human protein kinase SGK223.	952	46
1725	AAF24498 aal	Homo sapiens	GEST Human PG-3 coding sequence.	4362	99
1725	LAB35401	Homo sapiens	GEST Human PG-3.	4355	99
1725	gi13396864	Homo sapiens	unnamed protein product	4355	99
1726	AAB42784	Homo sapiens	CURA- Human ORFX ORF2548 polypeptide sequence SEQ ID NO:5096.	817	99
1726	gi12224887	Homo sapiens	mRNA; cDNA DKFZp547H027 (from clone DKFZp547H027); complete cds.	817	99
1726	gi10438459	Homo sapiens	cDNA: FLJ22174 fis, clone HRC00767.	817	99
1727	gi16740566	Homo sapiens	Similar to hypothetical protein FLJ13087, clone MGC:15009 IMAGE:3536735, mRNA, complete cds.	1854	100
1727	AAB95297	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17525.	807	95
1727	gi10434941	Homo sapiens	cDNA FLJ13087 fis, clone NT2RP3002099.	807	95
1728	AAB94075	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14267.	3506	97
1728	AAM93995	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 59.	3506	97
1728	gi14042145	Homo sapiens	cDNA FLJ14550 fis, clone NT2RM2001696.	3506	97
1729	AAG00897	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4978.	392	93
1729	AAG00898	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4979.	130	100
1729	AAB42597	Homo sapiens	CURA- Human ORFX ORF2361 polypeptide sequence SEQ ID NO:4722.	130	100
1730	ABB11613	Homo sapiens	HYSE- Human sorting nexin 7 homologue, SEQ ID NO:1983.	2341	100
1730	AAG74174	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4938.	2309	99
1730	gi4884241	Homo sapiens	mRNA; cDNA DKFZp564F052 (from clone DKFZp564F052); partial cds.	2148	99
1731	gi13445660	Homo sapiens	MP19(LIM2) mRNA, complete cds, alternatively spliced.	933	100
1731	gi11177546	Homo sapiens	LIM2 (LIM2) and natural killer group 7 (NKG7) genes, complete cds.	933	100
1731	gi13445658	Homo sapiens	MP19ins (LIM2) mRNA, complete cds, alternatively	880	80



SEQ ID	Hit ID	Species	Description	S score	Percent identity
			spliced.		
1732	AAB40591	Homo sapiens	CURA- Human ORFX ORF355 polypeptide sequence SEQ ID NO:710.	1056	100
1732	gi15617458	Oryctolagus cuniculus	Rab11 family interacting protein	869	48
1732	AA Y29488	Homo sapiens	CORI- Human lung tumour protein LT86-7 predicted amino acid sequence.	557	87
1733	gi10437750	Homo sapiens	cDNA: FLJ21616 fis, clone COL07477.	1680	99
1733	gi14349360	Homo sapiens	Similar to hypothetical protein FLJ21616, clone MGC:14941 IMAGE:3947903, mRNA, complete cds.	1443	99
1733	gi12805473	Mus musculus	Unknown (protein for IMAGE:3490304)	1410	97
1734	gi10437750	Homo sapiens	cDNA: FLJ21616 fis, clone COL07477.	1645	92
1734	gi14349360	Homo sapiens	Similar to hypothetical protein FLJ21616, clone MGC:14941 IMAGE:3947903, mRNA, complete cds.	1565	99
1734	gi12805473	Mus musculus	Unknown (protein for IMAGE:3490304)	1412	96
1735	AAB95036	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16791.	863	100
1735	gi10433448	Homo sapiens	cDNA FLJ12060 fis, clone HEMBB1002142.	863	100
1735	gi15341904	Homo sapiens	clone MGC:21051 IMAGE:4476886, mRNA, complete cds.	751	99
1736	gi14043783	Homo sapiens	clone MGC:14256 IMAGE:4129368, mRNA, complete cds.	2232	100
1736	gi10436857	Homo sapiens	cDNA: FLJ20897 fis, clone ADKA03573.	2232	100
1736	gi12653785	Homo sapiens	clone IMAGE:3349601, mRNA, partial cds.	1783	99
1737	gi14249850	Homo sapiens	clone MGC:15062 IMAGE:2959567, mRNA, complete cds.	1535	99
1737	AAM79539	Homo sapiens	HYSE- Human protein SEQ ID NO 3185.	1523	53
1737	AAM78555	Homo sapiens	HYSE- Human protein SEQ ID NO 1217.	1523	53
1738	gi13183338	Homo sapiens	calneuron 1 (CALN1) mRNA, complete cds.	881	100
1738	gi13183340	Mus musculus	calneuron 1	880	99
1738	gi7670344	Mus musculus	unnamed protein product	880	99
1739	gi4995927	Xenopus laevis	p33 ringo	545	49
1739	gi10280285	Xenopus sp.	unnamed protein product	545	49
1739	gi4446879	Xenopus laevis	speedy protein	540	48

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	0				
1740	gi15281553	Homo sapiens	solute carrier family 12 member 8 (SLC12A8) gene, partial cds.	1905	80
1740	gi17224940	Mus musculus	cation-chloride cotransporter	1761	74
1740	gi10439794	Homo sapiens	cDNA: FLJ23188 fis, clone LNG12038.	1613	99
1741	gi6330163	Homo sapiens	mRNA for KIAA1161 protein, partial cds.	1137	99
1741	gi7301333	Drosophila melanogaster	CG11909 gene product	485	41
1741	gi64404	Torpedo californica	4-acetamido-4'-isothiocyanostilbene-2, 2'-disulphonic acid-binding protein	415	38
1742	AAM67857	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 28163.	1553	100
1742	AAM55471	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 27576.	1553	100
1742	gi15620849	Homo sapiens	mRNA for KIAA1895 protein, partial cds.	1553	100
1743	gi2852640	Homo sapiens	clone 23856 unknown mRNA, partial cds.	942	99
1743	gi13325281	Homo sapiens	hypothetical protein MGC2683, clone MGC:4313 IMAGE:2819900, mRNA, complete cds.	700	100
1743	gi12654485	Homo sapiens	clone MGC:2683 IMAGE:2819900, mRNA, complete cds.	700	100
1744	gi13938307	Homo sapiens	clone MGC:15626 IMAGE:3343642, mRNA, complete cds.	526	62
1744	AAB90765	Homo sapiens	NOJ1/ Human shear stress-response protein SEQ ID NO: 30.	524	64
1744	AAB62159	Homo sapiens	NEUR- Human arginine-rich protein.	524	64
1745	gi7243207	Homo sapiens	mRNA for KIAA1413 protein, partial cds.	7273	99
1745	AAB93057	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11862.	3014	99
1745	gi7022861	Homo sapiens	cDNA FLJ10680 fis, clone NT2RP2006573, weakly similar to 2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37).	3014	99
1746	gi7243207	Homo sapiens	mRNA for KIAA1413 protein, partial cds.	7245	98
1746	AAB93057	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11862.	3014	99
1746	gi7022861	Homo sapiens	cDNA FLJ10680 fis, clone NT2RP2006573, weakly similar to 2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37).	3014	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1747	AAE10330	Homo sapiens	INCY- Human transporter and ion channel-7 (TRICH-7) protein.	1520	100
1747	AAM39422	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2567.	694	48
1747	AAM79397	Homo sapiens	HYSE- Human protein SEQ ID NO 3043.	694	48
1748	gi10439744	Homo sapiens	cDNA: FLJ23151 fis, clone LNG09417.	2362	100
1748	gi12860456	Mus musculus	putative	1732	70
1748	gi8954063	Arabidopsis thaliana	Contains similarity to a transposable element Tip100 protein for transposase from Ipomoea purpurea gb 4063769 and is a member of the transmembrane 4 family PF00335.	308	24
1749	gi17529987	Homo sapiens	oxysterol-binding protein-like protein OSBPL3 (OSBPL3) mRNA, complete cds.	4671	100
1749	gi17389382	Homo sapiens	oxysterol binding protein-like 3, clone MGC:21526 IMAGE:3909164, mRNA, complete cds.	4671	100
1749	gi10880973	Homo sapiens	oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds.	4671	100
1750	AAB94879	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16094.	2813	100
1750	gi10436338	Homo sapiens	cDNA FLJ13998 fis, clone Y79AA1002229, weakly similar to DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.	2813	100
1750	AAB94319	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14797.	2330	99
1751	AAB19390	Homo sapiens	LEXI- Amino acid sequence of a human lipoxigenase protein.	3836	100
1751	gi13378170	Homo sapiens	partial ALOXE3 gene for arachidonate lipoxigenase 3, exons 1 to 4B (and joined CDS).	3836	100
1751	gi10441004	Homo sapiens	epidermal lipoxigenase (ALOXE3) mRNA, complete cds.	3830	99
1752	AAM93241	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 2671.	664	95
1752	gi15030270	Homo sapiens	clone MGC:9889 IMAGE:3868330, mRNA, complete cds.	664	95
1752	AAO10285	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 24177.	486	78
1753	gi456191	Homo sapiens	H.sapiens mRNA for rho GDP-dissociation Inhibitor 1.	818	99
1753	gi337395	Homo sapiens	Human GDP dissociation inhibitor mRNA, complete cds.	818	99
1753	gi285979	Homo sapiens	Human rho GDI mRNA, complete cds.	818	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1754	AAQ43549_aa1	Homo sapiens	HARD Gamma subunit of human retinal cGMP phosphodiesterase DNA	472	100
1754	AAR93117	Homo sapiens	HARD cGMP-phosphodiesterase gamma-subunit.	472	100
1754	AAR38484	Homo sapiens	HARD Gamma subunit of human retinal cGMP phosphodiesterase.	472	100
1755	AAV19446	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	590	98
1755	AAV19599	Homo sapiens	HUMA- SEQ ID NO 317 from WO9922243.	590	98
1755	AAV19602	Homo sapiens	HUMA- SEQ ID NO 320 from WO9922243.	137	100
1756	gi10437393	Homo sapiens	cDNA: FLJ21313 fis, clone COL02176.	2197	99
1756	gi14250321	Homo sapiens	hypothetical protein FLJ21313, clone MGC:16820 IMAGE:4148772, mRNA, complete cds.	2193	99
1756	gi12858526	Mus musculus	putative	1936	86
1757	gi7414351	Homo sapiens	Hox1.8 gene for homeobox protein.	478	100
1757	gi2789672	Homo sapiens	homeobox protein A10 (HOXA10) gene, complete cds.	478	100
1757	gi15559235	Homo sapiens	clone MGC:12859 IMAGE:4107013, mRNA, complete cds.	478	100
1758	gi189772	Homo sapiens	Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.	872	90
1758	gi13543568	Homo sapiens	prostaglandin D2 synthase (21kD, brain), clone MGC:14559 IMAGE:4294999, mRNA, complete cds.	872	90
1758	gi12963879	Homo sapiens	prostaglandin D synthase mRNA, complete cds.	872	90
1759	gi2982508	Homo sapiens	mRNA for TCR beta chain, specific for Mage 3/HLA-A2.	1296	92
1759	gi3002925	Homo sapiens	T cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds.	1286	92
1759	gi36733	Homo sapiens	H.sapiens mRNA for T-cell antigen receptor beta-chain.	1047	75
1760	AAM25728	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1243.	667	99
1760	gi15529064	Homo sapiens	sorting nexin 14 (SNX14) mRNA, complete cds.	667	99
1760	gi13477273	Homo sapiens	clone MGC:13217 IMAGE:3959086, mRNA, complete cds.	667	99
1761	AAB94843	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16018.	1761	100
1761	gi10436267	Homo sapiens	cDNA FLJ13955 fis, clone Y79AA1001177.	1761	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1761	gi16339295	Mus musculus	Similar to hypothetical protein FLJ13955	1681	85
1762	AAE01058	Homo sapiens	HUMA- Human four disulfide core domain (FDCD)-containing protein.	1200	84
1762	gi12835376	Mus musculus	putative	918	68
1762	gi12655452	Homo sapiens	mRNA for keratin associated protein 4.7 (KRTAP4.7 gene).	892	68
1763	AAG67485	Homo sapiens	LEXI- Amino acid sequence of a human transporter protein.	2391	99
1763	AAE10333	Homo sapiens	INCY- Human transporter and ion channel-10 (TRICH-10) protein.	2368	96
1763	gi12718201	Homo sapiens	Human DNA sequence from clone RP11-305P22 on chromosome 20 Contains ESTs, STSs, GSSs and 7 CpG islands. Contains three novel genes and a novel gene for a helix-loop-helix DNA binding protein, complete sequence.	2243	100
1764	gi15778948	Homo sapiens	Similar to thiamine pyrophosphokinase, clone MGC:14885 IMAGE:3622116, mRNA, complete cds.	717	100
1764	gi12667203	Homo sapiens	thiamine pyrophosphokinase (TPK1) mRNA, complete cds.	717	100
1764	gi12248915	Homo sapiens	hTPK1 mRNA for thiamin pyrophosphokinase, complete cds.	717	100
1765	gi10438831	Homo sapiens	cDNA: FLJ22439 fis, clone HRC09236.	2525	99
1765	AAB42237	Homo sapiens	CURA- Human ORFX ORF2001 polypeptide sequence SEQ ID NO:4002.	2084	99
1765	gi13559284	Homo sapiens	Human DNA sequence from clone RP5-117516 on chromosome 20. Contains the 3' end of the gene for Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein), the 5' end of the gene encoding N-terminal acetyltransferase complex arl1 subunit, ESTs, STSs, GSSs and two CpG islands, complete sequence.	829	36
1766	gi9588428	Homo sapiens	Human DNA sequence from clone RP5-1024N4 on chromosome 1p32.1-33. Contains the gene for a novel Sodium:solute symporter family member similar to SLC5A1 (SGLT1), a pseudogene similar to part of butyrophilin family members, a novel gene, ESTs, STSs, GSSs and a putative CpG	2858	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			island, complete sequence.		
1766	gi529056	Homo sapiens	Na <sup>+</sup> /glucose cotransporter (SGLT1) gene, exon 15 and complete cds.	1955	55
1766	gi3646043	Homo sapiens	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contains ESTs and STSs, complete sequence.	1955	55
1767	AAB73485	Homo sapiens	MILL- Human aminopeptidase 22196.	3657	99
1767	gi12583612	Homo sapiens	mRNA for neurolysin.	3657	99
1767	gi13922467	Homo sapiens	unnamed protein product	3657	99
1768	gi10122138	Rattus norvegicus	SynGAP-a	6651	99
1768	gi2935448	Rattus norvegicus	synaptic ras GTPase-activating protein p135 SynGAP	6634	99
1768	gi6624587	Homo sapiens	Human DNA sequence from clone RP4-570F3 on chromosome 6. Contains the 5' end of the gene for the ortholog of the rat synaptic ras GTPase-activating protein p135 SynGAP, gene LOC51596 for divalent cation tolerant protein CUTA or brain acetylcholinesterase putative membrane anchor, the PHF1 gene for PHD finger protein 1, the KNSL2 gene for kinesin-like protein 2, the gene for a novel protein similar to ribosomal protein L12 (RPL12) and the gene for a novel protein similar to lysophospholipase II (LYPLA2). Contains ESTs, STSs, GSSs and four CpG islands, complete sequence.	6194	100
1769	AAB95863	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18931.	1040	100
1769	gi17389283	Homo sapiens	hypothetical protein FLJ14346, clone MGC:21027 IMAGE:4415420, mRNA, complete cds.	1040	100
1769	gi10436791	Homo sapiens	cDNA FLJ14346 fis, clone THYRO1001320.	1040	100
1770	AAB94517	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15235.	2593	99
1770	gi10435122	Homo sapiens	cDNA FLJ13203 fis, clone NT2RP3004504, highly similar to M.musculus mRNA for CPEB	2593	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			protein.		
1770	gi12659216	Homo sapiens	cytoplasmic polyadenylation element-binding protein short form (CPEB1) mRNA, complete cds.	2583	98
1771	AAB48059	Homo sapiens	INCY- Human extracellular signaling molecule (EXCS) (ID 1493630CD1).	432	97
1771	AAY36090	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 475.	420	95
1771	AAY11768	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No: 368.	257	95
1772	AAB93075	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11902.	2936	99
1772	gi14042415	Homo sapiens	cDNA FLJ14710 fis, clone NT2RP3000632, weakly similar to ZINC FINGER PROTEIN 84.	2936	99
1772	gi16551429	Homo sapiens	cDNA FLJ31551 fis, clone NT2RI2001083, moderately similar to ZINC FINGER PROTEIN 84.	1813	63
1773	AAY76843	Homo sapiens	INCY- Human proton ATPase subunit (HPAS) protein sequence.	356	100
1773	AAY88590	Homo sapiens	SATO/ Human tumour specific antigen amino acid sequence.	356	100
1773	AAW64534	Homo sapiens	SAGA Human fibrosarcoma cell line HT-1080 clone HP00442 protein.	356	100
1774	gi12407385	Homo sapiens	tripartite motif protein TRIM5 isoform gamma (TRIM5) mRNA, complete cds; alternatively spliced.	1818	99
1774	gi12407387	Homo sapiens	tripartite motif protein TRIM5 isoform delta (TRIM5) mRNA, complete cds; alternatively spliced.	1559	99
1774	gi12407383	Homo sapiens	tripartite motif protein TRIM5 isoform beta (TRIM5) mRNA, complete cds; alternatively spliced.	1557	100
1775	gi14250601	Homo sapiens	hypothetical protein FLJ22056, clone MGC:3045 IMAGE:3343082, mRNA, complete cds.	2600	99
1775	gi10438315	Homo sapiens	cDNA: FLJ22056 fis, clone HEP09916.	1747	100
1775	gi7295293	Drosophila melanogaster	CG8633 gene product	597	31
1776	gi10437059	Homo sapiens	cDNA: FLJ21054 fis, clone CAS00538.	736	100
1776	gi11558099	Mus musculus	syncoilin	653	89
1776	gi12835405	Mus musculus	putative	552	84
1777	gi163076	Homo sapiens	hypothetical protein FLJ12270,	3045	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	08		clone MGC:10176 IMAGE:3908004, mRNA, complete cds.		
1777	gi156209 05	Homo sapiens	mRNA for KIAA1923 protein, partial cds.	3042	99
1777	AAB939 45	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13963.	2190	100
1778	gi795981 9	Homo sapiens	PRO1430	299	100
1778	AAO078 40	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 21732.	75	54
1778	AAO088 70	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22762.	73	43
1779	AAG629 10	Homo sapiens	KLEE/ Amino acid sequence of a human xylosyltransferase (XT) isoform XT-II.	4625	100
1779	gi113222 70	Homo sapiens	mRNA for xylosyltransferase II (XT-II gene).	4625	100
1779	gi152096 53	Homo sapiens	human XT-II	4625	100
1780	gi992997 3	Macaca fascicularis	hypothetical protein	1778	96
1780	AAG787 40	Homo sapiens	BODE- Human transcriptional elongation factor IIS 24.	1162	99
1780	ABB1122 0	Homo sapiens	HYSE- Human TFIIIS homologue, SEQ ID NO:1590.	653	100
1781	gi152778 46	Homo sapiens	Similar to hypothetical protein FLJ21522, clone MGC:16817 IMAGE:3853503, mRNA, complete cds.	3122	99
1781	AAB643 72	Homo sapiens	INCY- Amino acid sequence of human intracellular signalling molecule INTRA4.	3100	99
1781	gi104376 38	Homo sapiens	cDNA: FLJ21522 fis, clone COL05884.	2892	94
1782	AAB946 25	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15483.	2688	100
1782	gi104353 87	Homo sapiens	cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MUSCLE.	2688	100
1782	gi165518 77	Homo sapiens	cDNA FLJ31903 fis, clone NT2RP7004260, weakly similar to MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B.	2429	92
1783	gi105681 12	Homo sapiens	ALR-like protein mRNA, complete cds.	17050	100
1783	gi563007 7	Homo sapiens	PAC clone RP5-981O7 from 7q34-q36, complete sequence.	9606	100
1783	AAB422 30	Homo sapiens	CURA- Human ORFX ORF1994 polypeptide sequence SEQ ID NO:3988.	9583	99
1784	AAB688 76	Homo sapiens	INCY- Human RECAP polypeptide, SEQ ID NO: 6.	1895	85
1784	gi104381 74	Homo sapiens	cDNA: FLJ21952 fis, clone HEP04970.	1895	85
1784	gi169242	Homo sapiens	hypothetical protein FLJ21952,	1862	84



SEQ ID	Hit ID	Species	Description	S score	Percent identity
	96		clone MGC:2790 IMAGE:2960984, mRNA, complete cds.		
1785	AAU160 26	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 979.	1433	100
1785	gi140178 23	Homo sapiens	mRNA for KIAA1803 protein, partial cds.	1433	100
1785	AAG780 55	Homo sapiens	GEAT Human zinc finger domain DNA binding protein S 1-3.	1168	99
1786	AAG004 05	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4486.	397	98
1786	AAM906 02	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:18195.	215	56
1786	AAM411 14	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6045.	84	34
1787	AAG020 95	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6176.	302	100
1787	gi665103 7	Mus musculus domesticus	similar to RNA binding protein	222	53
1787	gi128478 83	Mus musculus	putative	222	53
1788	gi979845 2	Homo sapiens	mRNA for putative capacitative calcium channel (trp7 gene).	4470	100
1788	gi532685 4	Mus musculus	receptor-activated calcium channel	4392	98
1788	gi229590 3	Homo sapiens	Human putative calcium influx channel (htrp3) mRNA, complete cds.	3529	81
1789	AAG023 37	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6418.	377	98
1789	AAM008 75	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 351.	72	31
1789	gi166669 2	Mus musculus	alpha-NAC, muscle-specific form gp220	72	34
1790	AAB733 81	Homo sapiens	NANF- Human gas vesicle protein homologue hGvpT-b.	2838	99
1790	gi120055 09	Homo sapiens	HT025 mRNA, complete cds.	2838	99
1790	gi173914 58	Homo sapiens	clone MGC:2462 IMAGE:2964737, mRNA, complete cds.	1699	99
1791	AAV994 38	Homo sapiens	GETH Human PRO1555 (UNQ763) amino acid sequence SEQ ID NO:338.	1300	100
1791	AAB240 37	Homo sapiens	GETH Human PRO1555 protein sequence SEQ ID NO:49.	1300	100
1791	gi126542 33	Homo sapiens	Similar to hypothetical protein, clone 1-2, clone MGC:5442 IMAGE:3449979, mRNA, complete cds.	1300	100
1792	AAB638 60	Homo sapiens	LUDW- Human prostate cancer associated antigen protein sequence SEQ ID NO:1222.	297	50
1792	AAM767 71	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein	272	51

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			SEQ ID NO: 37077.		
1792	AAM639 51	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 36056.	272	51
1793	AAB942 49	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14645.	799	99
1793	gi104343 56	Homo sapiens	cDNA FLJ12700 fis, clone NT2RP1000721.	799	99
1793	ABB1242 2	Homo sapiens	HYSE- Human bone marrow expressed protein SEQ ID NO: 261.	528	99
1794	AAB651 89	Homo sapiens	GETH Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.	1858	99
1794	AAB875 36	Homo sapiens	GETH Human PRO1013.	1858	99
1794	AAY666 66	Homo sapiens	GETH Membrane-bound protein PRO1013.	1858	99
1795	AAB651 89	Homo sapiens	GETH Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.	1655	93
1795	AAB875 36	Homo sapiens	GETH Human PRO1013.	1655	93
1795	AAY666 66	Homo sapiens	GETH Membrane-bound protein PRO1013.	1655	93
1796	gi777026 3	Homo sapiens	PRO3077	620	100
1796	gi158916 32	Agrobacterium tumefaciens	AGR_L_3035p	67	31
1797	AAY362 33	Homo sapiens	HUMA- Human secreted protein encoded by gene 10.	302	96
1797	gi298307	Rattus sp.	beta 3-adrenergic receptor; beta 3-AR	83	38
1797	gi241216	Rattus sp.	beta 3-adrenergic receptor	83	38
1798	ABB1203 7	Homo sapiens	HYSE- Human ribosomal protein L31 homologue, SEQ ID NO:2407.	341	100
1798	AAG038 94	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7975.	341	100
1798	AAB437 07	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1152.	341	100
1799	AAE1099 5	Homo sapiens	INCY- Human lipid metabolism enzyme-4 (LME-4) protein.	2242	99
1799	AAB419 89	Homo sapiens	CURA- Human ORFX ORF1753 polypeptide sequence SEQ ID NO:3506.	2224	98
1799	AAB940 07	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14123.	1212	99
1800	AAY761 94	Homo sapiens	HUMA- Human secreted protein encoded by gene 71.	296	98
1800	AAY131 96	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 210.	291	96
1800	AAY194 71	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	148	96
1801	ABB1242	Homo sapiens	HYSE- Human bone marrow	2841	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	2		expressed protein SEQ ID NO: 261.		
1801	gi3638956	Homo sapiens	PAC clone RP4-751H13 from 7q35-qter, complete sequence.	2830	100
1801	gi7670496	Mus musculus	unnamed protein product	2352	84
1802	AAU12382	Homo sapiens	GETH Human PRO792 polypeptide sequence.	1332	86
1802	AAB24416	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:155.	1332	86
1802	AAB24055	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:31.	1332	86
1803	AAU12382	Homo sapiens	GETH Human PRO792 polypeptide sequence.	1590	100
1803	AAB24416	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:155.	1590	100
1803	AAB24055	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:31.	1590	100
1804	AAB43713	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1158.	414	98
1804	AAR11490	Homo sapiens	CALI- Tissue-plastin.	414	98
1804	gi339848	Homo sapiens	Human T-plastin mRNA, 5' end.	414	98
1805	AAV19456	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	307	90
1805	gi13882500	Mycobacterium tuberculosis CDC1551	conserved hypothetical transmembrane protein	70	32
1805	gi1550714	Mycobacterium tuberculosis H37Rv	hypothetical protein Rv2673	70	32
1806	gi16552850	Homo sapiens	cDNA FLJ32676 fis, clone TEST1000168, weakly similar to PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.	1265	100
1806	gi12859936	Mus musculus	putative	962	78
1806	AAM38877	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2022.	200	45
1807	AAV41390	Homo sapiens	HUMA- Human secreted protein encoded by gene 83 clone HRAAB15.	813	100
1807	AAM39990	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3135.	581	44
1807	AAM38999	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2144.	581	44
1808	gi12836197	Mus musculus	putative	2154	75
1808	AAM82398	Homo sapiens	HUMA- Human immunc/haematopoietic antigen SEQ ID NO:9991.	750	90
1808	AAG04069	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 8150.	491	100
1809	AAB95252	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17419.	3112	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1809	gi10434729	Homo sapiens	cDNA FLJ12949 fis, clone NT2RP2005336, weakly similar to TRICHOHYALIN.	3112	99
1809	gi12804075	Homo sapiens	hypothetical protein FLJ12949, clone MGC:11261 IMAGE:3942403, mRNA, complete cds.	1786	100
1810	AAAY19587	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	160	96
1811	gi15620881	Homo sapiens	mRNA for KIAA1911 protein, partial cds.	1153	100
1811	AAM91641	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:19234.	326	50
1811	gi12845802	Mus musculus	putative	309	58
1812	gi10439911	Homo sapiens	cDNA: FLJ23282 fis, clone HEP07626.	2677	100
1812	AAAY99653	Homo sapiens	INCY- Human GTPase associated protein-4.	2324	100
1812	gi1016712	Rattus norvegicus	Fos-related antigen	2060	84
1813	AAAY60152	Homo sapiens	META- Human endometrium tumour EST encoded protein 212.	379	100
1813	AAAY60151	Homo sapiens	META- Human endometrium tumour EST encoded protein 211.	83	73
1813	AAB92984	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11704.	71	32
1814	gi14602995	Homo sapiens	hypothetical protein FLJ23375, clone MGC:16634 IMAGE:4121449, mRNA, complete cds.	2299	100
1814	gi104440040	Homo sapiens	cDNA: FLJ23375 fis, clone HEP16206.	2294	99
1814	AAB42973	Homo sapiens	CURA- Human ORFX ORF2737 polypeptide sequence SEQ ID NO:5474.	725	98
1815	AAM78722	Homo sapiens	HYSE- Human protein SEQ ID NO 1384.	1808	99
1815	gi15053987	Homo sapiens	c-Mpl binding protein mRNA, complete cds.	1439	100
1815	AAE10199	Homo sapiens	HYSE- Human bone marrow derived contig polypeptide, SEQ ID NO: 64.	1231	85
1816	gi10440474	Homo sapiens	mRNA for FLJ00074 protein, partial cds.	1001	100
1816	gi7020969	Homo sapiens	cDNA FLJ20703 fis, clone KAIA1965.	546	63
1816	gi13325142	Homo sapiens	DKFZP586I2223 protein, clone MGC:10840 IMAGE:3616057, mRNA, complete cds.	535	58
1817	gi10047249	Homo sapiens	mRNA for KIAA1587 protein, partial cds.	5002	100
1817	gi13676486	Macaca fascicularis	hypothetical protein	4641	92

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1817	gi12659140	Mus musculus	mage-e1	2474	67
1818	AAAY72596	Homo sapiens	ZYMO Human cytokine alpha protein-27 (Zalpha27).	3538	99
1818	gi12710297	Homo sapiens	unnamed protein product	3538	99
1818	gi10437588	Homo sapiens	cDNA: FLJ21478 fis, clone COL05012.	2793	100
1819	gi12838732	Mus musculus	putative	1060	91
1819	gi6572215	Homo sapiens	Human DNA sequence from clone RP1-37E16 on chromosome 22 Contains the 3' part of the gene for a novel VHS domain containing protein similar to predicted worm and human proteins, the SH3BP1 gene for SH3-domain binding protein 1, the gene for a novel protein similar to nitrophenylphosphatases from various organisms, the LGALS1 gene for soluble galactoside-binding lectin 1, a novel gene and the gene for a novel protein similar to mouse RIP3 (P116 Rho-interacting protein) and rat RB109, complete sequence.	647	46
1819	gi12653107	Homo sapiens	hypothetical protein dJ37E16.5, clone MGC:8472 IMAGE:2821743, mRNA, complete cds.	647	46
1820	AAB73690	Homo sapiens	INCY- Human oxidoreductase protein ORP-23.	2502	100
1820	gi10438222	Homo sapiens	cDNA: FLJ21988 fis, clone HEP06320.	2502	100
1820	gi14336719	Homo sapiens	16p13.3 sequence section 3 of 8.	2431	90
1821	gi3724105	Homo sapiens	hHa4 gene for keratin type I.	2029	99
1821	gi3724101	Homo sapiens	hHa3-I gene for keratin type I.	1798	90
1821	gi12852606	Mus musculus	putative	1796	87
1822	gi3228237	Homo sapiens	UHS KerB gene.	1079	88
1822	AAM79404	Homo sapiens	HYSE- Human protein SEQ ID NO 3050.	877	81
1822	gi200962	Mus musculus	serine 1 ultra high sulfur protein	867	70
1823	AAB86364	Homo sapiens	MEMO- Human ceramidase K2 protein.	1459	100
1823	AAB18986	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	1459	100
1823	gi14669436	Homo sapiens	alkaline phytoceramidase (APHC) mRNA, complete cds.	1459	100
1824	AAW61601	Homo sapiens	INCY- Human metallothionein HMBP-I.	381	98

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1824	AAB57183	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1761.	363	84
1824	AAO13869	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 27761.	362	81
1825	gi15928896	Homo sapiens	Similar to synaptotagmin-like 4, clone MGC:17313 IMAGE:3908307, mRNA, complete cds.	3496	100
1825	gi17385944	Rattus norvegicus	granuphilin A	3225	91
1825	gi5926736	Mus musculus	granuphilin-a	3187	90
1826	gi12653147	Homo sapiens	signal sequence receptor, beta (translocon-associated protein beta), clone MGC:8566 IMAGE:2822983, mRNA, complete cds.	864	99
1826	gi452757	Homo sapiens	H.sapiens mRNA for TRAP beta subunit.	847	99
1826	gi1736880	Homo sapiens	Human SSR2 mRNA for beta-signal sequence receptor, complete cds.	847	99
1827	AAB42722	Homo sapiens	CURA- Human ORFX ORF2486 polypeptide sequence SEQ ID NO:4972.	2865	100
1827	AAB95263	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17448.	2864	99
1827	gi10434759	Homo sapiens	cDNA FLJ12969 fis, clone NT2RP2005841, weakly similar to Homo sapiens mRNA for ALEX3.	2864	99
1828	gi7981297	Homo sapiens	Human DNA sequence from clone RP4-534K7 on chromosome 1p31.2-32.3. Contains the PGM1 gene for phosphoglucomutase 1, a novel gene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.	3323	100
1828	gi16041846	Homo sapiens	clone MGC:9635 IMAGE:3915942, mRNA, complete cds.	3308	99
1828	gi14017815	Homo sapiens	mRNA for KIAA1799 protein, partial cds.	3186	100
1829	gi9438033	Homo sapiens	scr/arg-rich pre-mRNA splicing factor SR-A1 (SR-A1) gene, complete cds.	6833	100
1829	gi10440402	Homo sapiens	mRNA for FLJ00034 protein, partial cds.	6827	99
1829	gi1438532	Rattus norvegicus	rA1	5019	82
1830	AAG81294	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:106.	1128	100
1830	AAU03589	Homo sapiens	INCY- Human DNA modification protein, DNAMP-4.	1128	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1830	gi17390202	Homo sapiens	Similar to RIKEN cDNA 2510005D08 gene, clone MGC:27120 IMAGE:4793121, mRNA, complete cds.	1128	100
1831	AAAY65282	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:1443.	472	95
1831	gi12838627	Mus musculus	putative	444	68
1831	gi6513867	Strongylocentrotus purpuratus	tektin A1	292	40
1832	AAAY10837	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	434	100
1832	gi7271606	Fowlpox virus	ORF FPV108 Virion envelope protein	72	28
1832	gi333523	Pigeonpox virus	major envelope antigen	72	28
1833	AAR56166	Homo sapiens	USSH Neuroendocrine tumor dlk.	2003	95
1833	gi15341994	Homo sapiens	clone MGC:17291 IMAGE:4347187, mRNA, complete cds.	2003	95
1833	gi15559310	Homo sapiens	clone MGC:20310 IMAGE:4130556, mRNA, complete cds.	2000	94
1834	AAM51465	Homo sapiens	TAKE Human G protein-coupled receptor protein TGR5.	1712	100
1834	AAAY86540	Homo sapiens	HUMA- Human gene 77-encoded protein fragment, SEQ ID NO:457.	679	98
1834	AAAY86291	Homo sapiens	HUMA- Human secreted protein HDPRK33, SEQ ID NO:206.	514	98
1835	gi16552598	Homo sapiens	cDNA FLJ32467 fis, clone SKNMC2000097, moderately similar to M.musculus mRNA for protein Htf9C.	2883	99
1835	gi15426494	Homo sapiens	HpaII tiny fragments locus 9C, clone MGC:14943 IMAGE:4054100, mRNA, complete cds.	2517	100
1835	gi10437555	Homo sapiens	cDNA: FLJ21453 fis, clone COL04585.	2517	100
1836	gi7243061	Homo sapiens	mRNA for KIAA1340 protein, partial cds.	2328	99
1836	gi3882143	Homo sapiens	mRNA for KIAA0711 protein, complete cds.	311	28
1836	gi14602992	Homo sapiens	clone MGC:16635 IMAGE:4121528, mRNA, complete cds.	309	29
1837	AAB94727	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15753.	2624	96
1837	gi10435806	Homo sapiens	cDNA FLJ13710 fis, clone PLACE2000373, weakly similar to F-SPONDIN PRECURSOR.	2624	96
1837	gi14250742	Homo sapiens	hypothetical protein FLJ13710, clone MGC:14171 IMAGE:4120678, mRNA, complete cds.	2473	98
1838	AAB199	Homo sapiens	INCY- Human oxidoreductase	1900	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	31		OXR-6.		
1838	gi17044356	Homo sapiens	unnamed protein product	1900	99
1838	AAW67737	Homo sapiens	REGC Human fsh05 gene protein product.	1528	100
1839	gi10440014	Homo sapiens	cDNA: FLJ23356 fis, clone HEP14919.	1859	99
1839	gi15208223	Macaca fascicularis	hypothetical protein	1798	96
1839	gi12853689	Mus musculus	putative	1535	80
1840	gi14250512	Homo sapiens	clone MGC:15468 IMAGE:2966921, mRNA, complete cds.	966	88
1840	gi14043262	Homo sapiens	Similar to RIKEN cDNA 1500026B10 gene, clone MGC:15737 IMAGE:3355622, mRNA, complete cds.	966	88
1840	gi12837754	Mus musculus	putative	710	68
1841	gi7671629	Homo sapiens	Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein (MOG), the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a CpG island, complete sequence.	2247	90
1841	gi431182	Mus musculus	Zfp-57	674	39
1841	gi14495650	Homo sapiens	zinc finger protein 331; zinc finger protein 463, clone MGC:15739 IMAGE:3355780, mRNA, complete cds.	444	29
1842	gi10439951	Homo sapiens	cDNA: FLJ23311 fis, clone HEP11681.	2175	99
1842	ABB12461	Homo sapiens	HYSE- Human bone marrow expressed protein SEQ ID NO: 300.	259	100
1842	gi5541722	Arabidopsis thaliana	putative protein	218	44
1843	gi9992884	Homo sapiens	vacuolar proton pump 116 kDa accessory subunit (ATP6N1B) mRNA, complete cds, alternatively spliced.	4378	100
1843	AAB60100	Homo sapiens	INCY- Human transport protein TPPT-20.	4331	99
1843	gi16903213	Mus musculus	H-ATPase accessory subunit a4	3809	85
1844	AAM93859	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3953.	3149	100
1844	gi17224957	Homo sapiens	cationic amino acid transporter (SLC7A3) mRNA, complete cds.	3149	100
1844	AAM933	Homo sapiens	HELI- Human polypeptide, SEQ	3142	99



SEQ ID	Hit ID	Species	Description	S score	Percent Identity
	85		ID NO: 2970.		
1845	gi12053007	Homo sapiens	mRNA; cDNA DKFZp434D1812 (from clone DKFZp434D1812); complete cds.	6038	99
1845	gi4240195	Homo sapiens	mRNA for KIAA0853 protein, partial cds.	4974	100
1845	AAB67047	Homo sapiens	INCY- Human immune response molecule (IMUN) protein SEQ ID NO: 1.	3777	99
1846	AAB94108	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14340.	2903	100
1846	AAU04557	Homo sapiens	GETH Human Stra6 homologue, PRO10282.	2903	100
1846	gi13560966	Homo sapiens	STRA6 isoform 1 mRNA, complete cds, alternatively spliced.	2903	100
1847	AAB58363	Homo sapiens	ROSE/ Lung cancer associated polypeptide sequence SEQ ID 701.	309	100
1847	AAY48507	Homo sapiens	META- Human breast tumour-associated protein 52.	308	98
1847	AAM23952	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1477.	294	98
1848	AAM93737	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3705.	929	49
1848	gi3170609	Rattus norvegicus	monocarboxylate transporter MCT3	631	35
1848	gi7670446	Mus musculus	unnamed protein product	631	47
1849	AAB95359	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17661.	3130	99
1849	gi10435088	Homo sapiens	cDNA FLJ13181 fis, clone NT2RP3004016, weakly similar to TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA.	3130	99
1849	gi7297357	Drosophila melanogaster	CG8419 gene product	746	29
1850	gi10436813	Homo sapiens	cDNA: FLJ20859 fis, clone ADKA01617.	2426	100
1850	gi13477183	Homo sapiens	Similar to hypothetical protein FLJ20859, clone MGC:12940 IMAGE:2822127, mRNA, complete cds.	2357	98
1850	gi12830810	Homo sapiens	false p73 target protein gene, complete cds.	2239	99
1851	AAM24367	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1892.	546	100
1851	AAY27576	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 10.	394	96
1851	gi30478	Homo sapiens	Human mRNA for dopamine beta-hydroxylase type b (EC 1.14.17.1).	68	26
1852	gi16551561	Homo sapiens	cDNA FLJ31657 fis, clone NT2RI2004304, moderately similar to Homo sapiens NY-	2859	92

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			REN-2 antigen mRNA.		
1852	AAB36626	Homo sapiens	INCY- Human FLEXHT-48 protein sequence SEQ ID NO:48.	2056	67
1852	gi12803469	Homo sapiens	high-glucose-regulated protein 8, clone MGC:7390 IMAGE:3139250, mRNA, complete cds.	2056	67
1853	gi7768736	Homo sapiens	genomic DNA, chromosome 21q, section 87/105.	4306	99
1853	gi14245729	Homo sapiens	ANKRD3 mRNA for dual-specificity Ser/Thr/Tyr kinase, complete cds.	4003	94
1853	gi9886711	Homo sapiens	mRNA for protein kinase (dik gene).	3999	94
1854	gi10439129	Homo sapiens	cDNA: FLJ22655 fis, clone HSI07590.	960	100
1854	AAG01459	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5540.	668	100
1854	AAU17365	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 930.	523	100
1855	gi10047185	Homo sapiens	mRNA for KIAA1560 protein, partial cds.	3397	100
1855	gi17512495	Mus musculus	glycerol-3-phosphate acyltransferase, mitochondrial	3371	93
1855	gi193367	Mus musculus	glycerol-3-phosphate acyltransferase	3363	93
1856	ABB12236	Homo sapiens	HYSE- Human eppin-1 homologue, SEQ ID NO:2606.	472	100
1856	gi13937334	Homo sapiens	Human DNA sequence from clone RP3-461P17 on chromosome 20q12-13.2. Contains two novel genes, gene HE4 for Major Epididymis-specific protein E4 precursor (Epididymis Secretory protein E4), RPL5 (60S Ribosomal Protein L5), COX6C (Cytochrome C Oxidase subunit VIC) and HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL, HUCHA60) pseudogenes, the SPINT3 gene for Kunitz type serine protease inhibitor 3 (HKIB9), two genes for novel Kunitz/Bovine pancreatic trypsin inhibitor and WAP-type (Whey Acidic Protein) 'four-disulfide core' domains containing proteins and the gene for Eppin-1, -2 and -3. Contains ESTs, STSs, GSSs and a CpG island, complete sequence.	415	98
1856	gi13591753	Oryctolagus cuniculus	eppin	257	66

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1857	gi128558	Mus musculus	putative	758	57
1857	gi177366	Homo sapiens	Human DNA sequence from clone RP3-341D10 on chromosome X Contains a gene for a novel protein, part of the gene for a protein similar to ADP ribosylation factor 3, part of a gene similar to HTF9C and a CpG island, complete sequence.	424	100
1857	AAM38958	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2103.	421	43
1858	gi10439520	Homo sapiens	cDNA: FLJ22973 fis, clone KAT11042.	2289	100
1858	gi11612388	Homo sapiens	zinc finger transcription factor Pegasus mRNA, complete cds.	2279	99
1858	AAU16142	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1095.	1745	98
1859	gi13544026	Homo sapiens	putative zinc finger protein from EUROIMAGE 566589, clone MGC:13109 IMAGE:3959436, mRNA, complete cds.	1481	99
1859	AAB93932	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13929.	1474	99
1859	gi10433647	Homo sapiens	cDNA FLJ12222 fis, clone MAMMA1001105, moderately similar to OVO PROTEIN.	1474	99
1860	AAQ78615	Homo sapiens	SHAN- Human zinc finger transcription factor BioZTF45.	1760	89
1860	gi13623431	Homo sapiens	clone MGC:13132 IMAGE:4124255, mRNA, complete cds.	1753	100
1860	gi13111897	Homo sapiens	Similar to KIAA0414 protein, clone MGC:2629 IMAGE:3503643, mRNA, complete cds.	1753	100
1861	AAB62201	Homo sapiens	RIGE- Cell cycle protein Radh-isoform 1.	3697	99
1861	gi8163804	Mus musculus	putative repair and recombination helicase RAD26L	3215	89
1861	AAB62202	Homo sapiens	RIGE- Cell cycle protein Radh-isoform 2.	2142	99
1862	gi2598565	Mus musculus	rab19	1008	88
1862	AAM78977	Homo sapiens	HYSE- Human protein SEQ ID NO 1639.	603	56
1862	gi7295127	Drosophila melanogaster	Rab-RP3 gene product	523	55
1863	gi17384067	Homo sapiens	Human DNA sequence from clone RP11-146P21 on chromosome 10 Contains the 3'end of a novel gene, a novel gene, the 5'end of the gene for KIAA0608 and a CpG island, complete sequence.	2467	99
1863	gi140399	Cricetulus	hypothetical protein 1-2	2311	92

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	64	griscus			
1863	AAB95196	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17284.	2183	99
1864	gi12653987	Homo sapiens	cutaneous T-cell lymphoma tumor antigen sc70-2, clone MGC:5291 IMAGE:3451565, mRNA, complete cds.	1237	99
1864	gi11385662	Homo sapiens	CTCL tumor antigen sc70-2 mRNA, complete cds.	1237	99
1864	gi10436925	Homo sapiens	cDNA: FLJ20957 fis, clone ADSE02053.	1233	99
1865	gi10439911	Homo sapiens	cDNA: FLJ23282 fis, clone HEP07626.	2579	100
1865	AAAY99653	Homo sapiens	INCY- Human GTPase associated protein-4.	2544	100
1865	gi1016712	Rattus norvegicus	Fos-related antigen	2256	84
1866	AAB53073	Homo sapiens	GETH Human angiogenesis- associated protein PRO195, SEQ ID NO:46.	331	100
1866	AAB88428	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0203.	331	100
1866	AAU12307	Homo sapiens	GETH Human PRO195 polypeptide sequence.	331	100
1867	AAB94197	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14532.	4854	99
1867	gi10434243	Homo sapiens	cDNA FLJ12634 fis, clone NT2RM4001858, weakly similar to T-BOX CONTAINING PROTEIN TBX6L.	4854	99
1867	gi6692607	Mus musculus	MGA protein	4810	84
1868	AAB95779	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18726.	1326	100
1868	AAB42878	Homo sapiens	CURA- Human ORFX ORF2642 polypeptide sequence SEQ ID NO:5284.	1326	100
1868	gi10436625	Homo sapiens	cDNA FLJ14220 fis, clone NT2RP3003828.	1326	100
1869	AAAY10823	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	183	100
1869	gi1171584	Plasmodium falciparum	red algal chloroplast	72	29
1869	gi630468	Plasmodium falciparum	hypothetical protein 470 - Plasmodium falciparum >	72	29
1870	gi14336713	Homo sapiens	16p13.3 sequence section 3 of 8.	1867	100
1870	gi5912459	Homo sapiens	Human DNA sequence from clone LA16-380A1 on chromosome 16 Contains two novel genes, ESTs, an STS, GSSs and five putative CpG islands, complete sequence.	1106	100
1870	gi13905232	Mus musculus	Unknown (protein for IMAGE:3601186)	145	28
1871	AAB433	Homo sapiens	CURA- Human ORFX	2463	97

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	82		ORF3146 polypeptide sequence SEQ ID NO:6292.		9
1871	AAW73400	Homo sapiens	HUMA- Human secreted protein encoded by Gene No. 4.	2454	10
1871	AAB58340	Homo sapiens	ROSE/ Lung cancer associated polypeptide sequence SEQ ID 678.	2252	90
1872	AAB56924	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1502.	2048	95
1872	AAY59993	Homo sapiens	META- Human endometrium tumour EST encoded protein 53.	2048	95
1872	gi4761223	Homo sapiens	NADP+-dependent isocitrate dehydrogenase (PICD) mRNA, complete cds.	2048	95
1873	AAB64373	Homo sapiens	INCY- Amino acid sequence of human intracellular signalling molecule INTRA5.	1875	100
1873	AAB94937	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16430.	1546	99
1873	gi15291919	Drosophila melanogaster	LD31969p	1237	41
1874	AAB64373	Homo sapiens	INCY- Amino acid sequence of human intracellular signalling molecule INTRA5.	1836	92
1874	AAB94937	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16430.	1546	99
1874	gi15291919	Drosophila melanogaster	LD31969p	1209	39
1875	gi13623511	Homo sapiens	clone MGC:12921 IMAGE:4129897, mRNA, complete cds.	590	100
1875	gi12698216	Macaca fascicularis	hypothetical protein	589	99
1875	AAM93616	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3444.	584	99
1876	gi6063688	Homo sapiens	ammecr1 gene, exon 1 and joined CDS (alternative transcripts).	968	56
1876	gi5139482	Homo sapiens	mRNA for AMMECR1 protein.	968	56
1876	gi8894657	Mus musculus	AMMECR1	964	53
1877	gi10440218	Homo sapiens	cDNA: FLJ23506 fis, clone LNG03055.	2913	99
1877	AAY73363	Homo sapiens	INCY- HTRM clone 2762174 protein sequence.	2110	100
1877	AAU16262	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1215.	1286	98
1878	AAG67151	Homo sapiens	INCY- Amino acid sequence of a human enzyme.	1689	99
1878	gi12856210	Mus musculus	putative	1457	85
1878	gi3128218	Arabidopsis thaliana	putative katanin	874	56
1879	AAB60093	Homo sapiens	INCY- Human transport protein TPPT-13.	3295	95

SEQ ID	Hit ID	Species	Description	S score	Percent Identity
1879	gi17223724	Homo sapiens	sodium/glucose cotransporter KST1 mRNA, complete cds.	3295	95
1879	AAF84023_aal	Homo sapiens	LEXI- Novel human transporter protein (NHP) encoding DNA.	3289	95
1880	AAB60093	Homo sapiens	INCY- Human transport protein TPPT-13.	3461	99
1880	gi17223724	Homo sapiens	sodium/glucose cotransporter KST1 mRNA, complete cds.	3461	99
1880	AAF84023_aal	Homo sapiens	LEXI- Novel human transporter protein (NHP) encoding DNA.	3455	99
1881	gi12845475	Mus musculus	putative	1648	70
1881	gi13543307	Homo sapiens	cargo selection protein (mannose 6 phosphate receptor binding protein), clone MGC:11117 IMAGE:3833411, mRNA, complete cds.	725	39
1881	AAY67240	Homo sapiens	INCY- Human adipophilin-like protein (HALP) amino acid sequence.	724	39
1882	AAW46904	Homo sapiens	ASAH A human mutant alanine aminotransferase.	1821	68
1882	gi1763096	Homo sapiens	Human glutamate pyruvate transaminase (GPT) gene, complete cds.	1821	68
1882	gi17390465	Homo sapiens	glutamic-pyruvate transaminase (alanine aminotransferase), clone MGC:17068 IMAGE:4179699, mRNA, complete cds.	1821	68
1883	AAD09495_aal	Homo sapiens	SUGE- Human SGP003 phosphatase polypeptide encoding DNA.	1161	100
1883	AAE04837	Homo sapiens	SUGE- Human SGP003 phosphatase polypeptide.	1159	99
1883	AAB18667	Homo sapiens	INCY- A human regulator of intracellular phosphorylation.	1021	91
1884	gi3089427	Homo sapiens	SSC6 rearranged T cell receptor beta chain (TCRBV17) gene, complete cds.	1089	69
1884	gi3002927	Homo sapiens	T cell receptor beta chain (TCRBV17S1-TCRBJ1S5) mRNA, complete cds.	1089	69
1884	gi2982508	Homo sapiens	mRNA for TCR beta chain, specific for Mage 3/HLA-A2.	1089	70
1885	gi12858221	Mus musculus	putative	1850	91
1885	gi12314102	Homo sapiens	Human DNA sequence from clone RP3-329L24 on chromosome 6q22.1-22.33 Contains a gene for a novel protein, part of a gene for a hypothetical 23.0 KD protein, part of a gene for a protein (MCM2/3/5 family), ESTs, STSs, GSSs and a CpG island, complete sequence.	1405	100
1885	gi438883	Arabidopsis	putative DNA replication	726	41

SEQ ID	Ht ID	Species	Description	S score	Percent identity
	2	thaliana	licensing factor		
1886	gi14714600	Homo sapiens	clone IMAGE:3354344, mRNA, partial cds.	3001	99
1886	AAR94386	Homo sapiens	NEWE- Human neural cell protein marker RR/B.	673	29
1886	gi3769362	Homo sapiens	ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.	673	29
1887	gi10047239	Homo sapiens	mRNA for KIAA1582 protein, partial cds.	7698	96
1887	gi16551820	Homo sapiens	cDNA FLJ31859 fis, clone NT2RP7001231.	3076	100
1887	gi7959181	Homo sapiens	mRNA for KIAA1460 protein, partial cds.	2840	45
1888	gi10047239	Homo sapiens	mRNA for KIAA1582 protein, partial cds.	7800	99
1888	gi16551820	Homo sapiens	cDNA FLJ31859 fis, clone NT2RP7001231.	2835	93
1888	gi7959181	Homo sapiens	mRNA for KIAA1460 protein, partial cds.	2744	44
1889	gi10047239	Homo sapiens	mRNA for KIAA1582 protein, partial cds.	7372	95
1889	gi7959181	Homo sapiens	mRNA for KIAA1460 protein, partial cds.	2618	44
1889	gi16551820	Homo sapiens	cDNA FLJ31859 fis, clone NT2RP7001231.	2354	81
1890	gi16307285	Homo sapiens	clone IMAGE:3877337, mRNA, partial cds.	1627	98
1890	gi15208051	Macaca fascicularis	hypothetical protein	1417	55
1890	AAAY94918	Homo sapiens	GEMY Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	1247	63
1891	gi2780414	Homo sapiens	hBACH mRNA for brain acyl-CoA hydrolase, complete cds.	1742	100
1891	gi16924333	Homo sapiens	cytosolic acyl coenzyme A thioester hydrolase, clone MGC:1126 IMAGE:3507488, mRNA, complete cds.	1742	100
1891	AAW74896	Homo sapiens	HUMA- Human secreted protein encoded by gene 169 clone HPTTU11.	1715	98
1892	AAB68874	Homo sapiens	INCY- Human RECAP polypeptide, SEQ ID NO: 4.	1266	100
1892	AAAY94890	Homo sapiens	PROT- Human protein clone HP02798.	1266	100
1892	gi14424518	Homo sapiens	Similar to RIKEN cDNA 1190004A01 gene, clone MGC:13153 IMAGE:4302257, mRNA, complete cds.	1266	100
1893	gi14595019	Homo sapiens	mRNA for keratin 6 1rs (KRT6IRS gene).	843	77
1893	gi6092075	Mus musculus	type II cytokeratin	836	74
1893	gi12834535	Mus musculus	putative	836	74
1894	gi14029153	Homo sapiens	microtubule-associated protein GLFND mRNA, complete cds.	2565	100

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1894	gi13111907	Homo sapiens	clone MGC:3213 IMAGE:3502614, mRNA, complete cds.	2565	100
1894	gi13447759	Homo sapiens	fibronectin type 3 and SPRY domain-containing protein 1 (FSD1) mRNA, complete cds.	2562	99
1895	gi14424591	Homo sapiens	hypothetical protein FLJ22127, clone MGC:14926 IMAGE:4123948, mRNA, complete cds.	2565	100
1895	gi10438086	Homo sapiens	cDNA: FLJ21886 fis, clone HEP03022.	2555	99
1895	gi10438400	Homo sapiens	cDNA: FLJ22127 fis, clone HEP19530.	1566	100
1896	gi15150306	Homo sapiens	glycogenin-interacting protein 3 mRNA, complete cds.	1571	100
1896	gi15150304	Homo sapiens	glycogenin-interacting protein 2 mRNA, complete cds, alternatively spliced.	1571	100
1896	gi15150298	Homo sapiens	glycogenin-interacting protein 1 mRNA, complete cds.	1571	100

**TABLE 3**

SEQ ID NO:	Database entry ID	Description	Results*
950	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 2.500e-20 267-285 BL00972D 22.55 5.179e-17 828-853 BL00972E 20.72 8.650e-13 855-877 BL00972C 16.48 7.120e-11 411-426 BL00972B 9.45 7.923e-10 353-363
950	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 8.000e-10 2-17
950	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.671e-09 5-20 PR00308A 5.90 9.471e-09 4-19
951	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.696e-09 331-344
951	PR00180	CELLULAR RETINALDEHYDE-BINDING PROTEIN SIGNATURE	PR00180C 10.92 8.821e-09 70-92
952	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.696e-09 331-344
952	PR00180	CELLULAR RETINALDEHYDE-BINDING PROTEIN SIGNATURE	PR00180C 10.92 8.821e-09 70-92
953	PR00401	SH2 DOMAIN SIGNATURE	PR00401B 12.94 1.000e-08 340-351
954	PR00401	SH2 DOMAIN SIGNATURE	PR00401B 12.94 1.000e-08 367-378
955	BL00625	Regulator of chromosome condensation (RCC1) proteins.	BL00625A 16.21 7.787e-16 308-337 BL00625A 16.21 7.369e-15 190-219 BL00625B 17.69 1.514e-13 302-336 BL00625B 17.69 2.286e-13 184-218 BL00625B 17.69 3.957e-13 132-166 BL00625A 16.21 5.690e-13 138-167 BL00625A 16.21 5.731e-11 360-389 BL00625B 17.69 3.333e-10 354-388



SEQ ID NO:	Database entry ID	Description	Results*
955	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633A 9.32 6.143e-09 202-219 PR00633H 15.10 6.268e-09 196-218 PR00633F 10.03 6.354e-09 373-388 PR00633G 13.71 7.556e-09 190-209
957	BL00120	Lipases, serine proteins.	BL00120B 11.37 9.486e-12 166-181
957	PR00111	ALPHA/BETA HYDROLASE FOLD SIGNATURE	PR00111B 10.61 1.176e-09 170-184
963	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.329e-10 45-93
966	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.034e-09 262-277
967	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.034e-09 74-89
968	BL00790	Receptor tyrosine kinase class V proteins.	BL00790D 12.41 8.297e-09 804-829
969	BL00790	Receptor tyrosine kinase class V proteins.	BL00790D 12.41 8.297e-09 878-903
971	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 2.080e-22 321-343 PR00380A 14.18 1.486e-21 79-101 PR00380B 12.64 6.571e-18 217-235 PR00380C 13.18 6.927e-13 269-288
971	BL00411	Kinesin motor domain proteins.	BL00411H 15.66 8.200e-30 320-351 BL00411G 21.39 6.100e-28 270-312 BL00411C 15.04 7.000e-22 79-101 BL00411F 14.77 1.273e-19 208-233 BL00411E 10.43 7.429e-12 142-161 BL00411A 11.31 4.484e-11 9-24 BL00411B 13.51 1.563e-10 45-62
971	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e-09 598-609
971	DM01399	VARICELLA-ZOSTER VIRUS GENE 54 PROTEIN.	DM01399B 12.42 7.092e-09 1571-1583

\*Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

SEQ ID NO:	Database entry ID	Description	Results*
971	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.800e-10 1350-1361 BL00678 9.67 7.158e-09 1629-1640
971	BL00502	Polygalacturonase proteins.	BL00502A 13.44 7.341e-09 1424-1439
971	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 7.796e-09 568-619
971	BL00226	Intermediate filaments proteins.	BL00226B 23.86 8.012e-09 930-978
971	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 2.385e-12 1348-1363 PR00320C 13.01 1.720e-10 1348-1363 PR00320A 16.74 4.971e-10 1348-1363 PR00320B 12.19 5.886e-10 1544-1559 PR00320A 16.74 3.415e-09 1544-1559 PR00320C 13.01 5.500e-09 1498-1513 PR00320B 12.19 8.650e-09 1627-1642 PR00320C 13.01 9.100e-09 1627-1642

SEQ ID NO:	Database entry ID	Description	Results*
973	BL01242	Formamidopyrimidine-DNA glycosylase proteins.	BL01242P 17.92 5.300e-11 32-66
975	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 2.500e-14 46-59
975	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 7.750e-11 371-385
976	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-09 99-132
977	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.250e-25 93-115 PR00380D 9.93 4.857e-19 302-324 PR00380B 12.64 4.429e-18 212-230 PR00380C 13.18 1.692e-16 247-266
977	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 7.750e-32 248-290 BL00411F 14.77 1.000e-25 203-228 BL00411C 15.04 1.621e-24 93-115 BL00411H 15.66 1.871e-24 301-332 BL00411E 10.43 6.625e-20 143-162 BL00411A 11.31 4.484e-11 5-20
977	PF00846	Hantavirus nucleocapsid protein.	PF00846H 3.96 9.182e-10 408-445
977	BL00224	Clathrin light chain proteins.	BL00224B 16.94 7.136e-09 363-416
978	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.368e-18 36-67
978	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 2.068e-10 36-55
980	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 9.376e-09 76-120
982	BL00790	Receptor tyrosine kinase class V proteins.	BL00790E 29.58 1.111e-12 614-662 BL00790E 29.58 3.111e-12 668-716 BL00790E 29.58 7.000e-10 560-608
982	BL00279	Membrane attack complex components / perforin proteins.	BL00279E 37.11 7.632e-12 727-775 BL00279E 37.11 2.047e-09 765-813
982	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 4.600e-11 791-807 BL01187B 12.04 3.571e-10 829-845 BL01187B 12.04 8.714e-10 753-769 BL01187A 9.98 4.375e-09 812-824 BL01187A 9.98 5.125e-09 774-786
982	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 5.364e-09 13-32
982	PR00764	COMPLEMENT C9 SIGNATURE	PR00764F 16.89 8.027e-10 744-765 PR00764F 16.89 6.844e-09 782-803
982	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010A 11.79 6.192e-11 814-826 PR00010C 11.16 5.909e-10 758-769 PR00010A 11.79 7.677e-10 776-788 PR00010C 11.16 1.214e-09 796-807 PR00010C 11.16 8.286e-09 834-845
986	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.150e-12 126-149
987	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 6.087e-10 93-107 PR00019B 11.36 7.840e-09 90-104

SEQ ID NO:	Database entry ID	Description	Results*
990	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.	PD01443D 8.36 4.670e-09 815-837
991	BL01101	Casein kinase II regulatory subunit proteins.	BL01101A 16.07 1.000e-40 9-54 BL01101B 10.94 9.000e-31 72-97
991	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE	PR00472C 12.38 5.154e-28 80-102 PR00472A 8.03 7.600e-23 8-25 PR00472B 14.84 1.000e-19 25-40
994	BL01166	RNA polymerases beta chain proteins.	BL01166G 18.10 2.500e-34 824-866 BL01166H 19.05 9.410e-30 936-986 BL01166D 17.37 4.396e-19 612-642 BL01166E 13.47 8.244e-17 682-706 BL01166C 12.21 9.357e-12 431-456
995	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 7.000e-09 25-34
996	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038A 13.61 6.625e-11 284-300
996	DM00984	w MYOD MYOBLAST DETERMINATION SHORT.	DM00984B 15.18 3.901e-09 262-317
996	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009A 13.75 7.750e-09 260-278
997	BL00905	GTP1/OBG family proteins.	BL00905D 15.00 4.214e-10 125-140
997	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 3.903e-13 63-86 PR00449A 13.20 7.750e-10 22-44
997	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.624e-10 56-96
997	BL01115	GTP-binding nuclear protein ran proteins.	BL01115B 10.81 1.505e-09 102-146
998	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 7.300e-15 64-80
998	BL00239	Receptor tyrosine kinase class II proteins.	BL00239E 17.14 2.693e-10 36-86
1001	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 5.263e-09 328-339
1003	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 5.263e-09 246-257
1004	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 5.263e-09 328-339
1010	BL00226	Intermediate filaments proteins.	BL00226B 23.86 5.919e-09 560-608
1012	PR00322	G10 PROTEIN SIGNATURE	PR00322E 6.62 1.720e-10 30-40
1012	BL00997	G10 protein.	BL00997C 6.36 3.308e-09 29-39
1013	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 110-139 BL00269A 8.53 2.607e-20 45-65 BL00269B 19.17 5.500e-17 72-101
1014	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e-10 6-60
1015	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.846e-11 476-493 BL00028 16.07 6.192e-11 989-1006
1015	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.087e-10 473-487 PR00048A 10.52 1.000e-09 986-1000
1015	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.571e-12 464-477 PD00066 13.92 7.000e-12 977-990 PD00066 13.92 4.600e-09 949-962 PD00066 13.92

SEQ ID NO:	Database entry ID	Description	Results*
			7.300e-09 397-410
1019	BL00289	Pentaxin family proteins.	BL00289E 18.00 4.375e-13 22-37
1019	PR00895	PENTAXIN SIGNATURE	PR00895G 14.55 4.913e-10 19-31
1022	BL00348	53 tumor antigen proteins.	BL00348F 23.19 4.571e-09 140-183
1023	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.684e-13 248-264
1023	PR00154	AMP-BINDING SIGNATURE	PR00154A 8.88 7.375e-10 241-253
1026	BL00421	Transmembrane 4 family proteins.	BL00421E 20.97 1.851e-09 17-47
1026	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259D 13.50 7.097e-09 20-47
1028	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.149e-29 6-45
1028	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.692e-15 234-247 PD00066 13.92 3.400e-14 150-163 PD00066 13.92 5.800e-14 206-219 PD00066 13.92 8.714e-12 178-191
1028	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.350e-13 102-119 BL00028 16.07 5.500e-11 190-207 BL00028 16.07 6.192e-11 218-235 BL00028 16.07 1.000e-09 134-151
1028	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.750e-14 215-229 PR00048A 10.52 5.500e-13 99-113 PR00048A 10.52 4.316e-11 131-145 PR00048B 6.02 4.462e-11 115-125 PR00048A 10.52 1.391e-10 159-173 PR00048B 6.02 6.625e-10 203-213 PR00048A 10.52 4.600e-09 187-201 PR00048B 6.02 8.579e-09 147-157
1029	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 2.059e-10 215-230
1029	BL00790	Receptor tyrosine kinase class V proteins.	BL00790F 15.90 2.519e-09 157-184
1032	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 133-162 BL00269A 8.53 2.607e-20 68-88 BL00269B 19.17 5.500e-17 95-124
1033	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 1.231e-20 75-128
1034	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.835e-11 326-359
1034	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 4.150e-11 112-126 PR00019B 11.36 8.000e-11 109-123 PR00019B 11.36 8.500e-11 184-198 PR00019A 11.19 6.478e-10 187-201 PR00019A 11.19 7.333e-09 63-77
1034	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 9.609e-09 334-344
1035	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 6.276e-12 358-376
1035	BL00567	Phosphoribulokinase proteins.	BL00567A 10.66 6.459e-11 360-

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			379
1038	BL00120	Lipases, serine proteins.	BL00120C 12.62 9.053e-12 95-106
1038	PR00825	VESPID VENOM ALLERGEN PHOSPHOLIPASE A1 SIGNATURE	PR00825B 14.81 1.371e-10 83-104
1038	PR00821	TRIACYLGLYCEROL LIPASE FAMILY SIGNATURE	PR00821E 9.64 4.896e-12 19-38 PR00821F 16.10 1.806e-09 118-134
1044	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.500e-30 169-212
1044	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 5.179e-16 197-215 BL00032B 10.83 3.060e-15 158-197
1044	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 8.071e-13 201-211 PR00024B 11.27 7.000e-12 191-202
1044	PR00026	ENGRAILED HOMEODOMAIN SIGNATURE	PR00026A 7.47 9.710e-12 153-171
1044	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.724e-10 192-209
1044	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 6.434e-10 155-171
1048	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.200e-14 7-41
1048	BL00211	ABC transporters family proteins.	BL00211A 12.23 4.600e-09 9-21
1049	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 1.783e-09 211-230 PR00014A 8.22 3.045e-09 373-383 PR00014C 15.44 6.087e-09 309-328
1049	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 1.750e-12 642-673 BL00790I 20.01 6.125e-12 320-351 BL00790I 20.01 6.679e-09 222-253
1049	PR00096	GLUTAMINE AMIDOTRANSFERASE SUPERFAMILY SIGNATURE	PR00096B 9.72 9.827e-09 689-701
1050	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372C 23.69 4.919e-12 67-103
1053	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-11 194-233
1053	PR00544	PROGESTERONE RECEPTOR SIGNATURE	PR00544F 7.76 3.329e-09 18-35
1057	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464A 20.47 9.591e-16 149-170 PR00464C 18.84 1.000e-15 324-353 PR00464D 17.40 6.250e-15 353-371 PR00464B 20.41 1.844e-12 205-224
1057	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385A 14.97 1.346e-12 335-353 PR00385B 10.22 4.130e-11 353-367
1057	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463E 17.37 4.814e-11 344-371
1058	PD02382	RECEPTOR CHAIN PRECURSOR TRANSME.	PD02382A 17.43 9.321e-09 99-115
1060	BL00795	Involucrin proteins.	BL00795C 17.06 6.442e-10 905-950
1060	BL00422	Granins proteins.	BL00422C 16.18 4.255e-10 910-938 BL00422C 16.18 4.353e-09

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			913-941
1060	PF00992	Troponin.	PF00992A 16.67 2.184e-09 900-935 PF00992A 16.67 5.382e-09 889-924
1060	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 7.429e-09 883-934
1060	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.326e-09 903-938
1063	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.644e-09 603-636
1063	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.643e-10 96-111 PR00049D 0.00 2.525e-09 95-110 PR00049D 0.00 3.898e-09 114-129 PR00049D 0.00 7.407e-09 97-112
1063	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 8.670e-09 100-112
1064	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-11 137-176
1064	PR00544	PROGESTERONE RECEPTOR SIGNATURE	PR00544F 7.76 3.329e-09 18-35
1065	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-11 187-226
1065	PR00544	PROGESTERONE RECEPTOR SIGNATURE	PR00544F 7.76 3.329e-09 18-35
1066	BL00218	Amino acid permeases proteins.	BL00218D 21.49 7.324e-11 226-271 BL00218E 23.30 3.475e-09 307-347
1067	BL00994	Bacterial export FHIPEP family proteins.	BL00994A 15.15 1.086e-09 71-118
1068	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.385e-33 6-45
1068	BL01030	RNA polymerases M / 15 Kd subunits proteins.	BL01030 23.44 7.480e-10 283-321
1068	BL00466	TFIIS zinc ribbon domain proteins.	BL00466 25.88 5.622e-09 283-320
1068	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.385e-15 271-284 PD00066 13.92 3.077e-15 243-256 PD00066 13.92 3.077e-15 320-333 PD00066 13.92 3.077e-15 348-361 PD00066 13.92 3.077e-15 376-389 PD00066 13.92 3.077e-15 432-445 PD00066 13.92 3.077e-15 617-630 PD00066 13.92 3.077e-15 701-714 PD00066 13.92 7.923e-15 215-228 PD00066 13.92 8.200e-14 589-602 PD00066 13.92 8.800e-14 729-742 PD00066 13.92 5.714e-12 542-555 PD00066 13.92 9.571e-12 561-574 PD00066 13.92 3.739e-11 404-417 PD00066 13.92 1.692e-10 299-312 PD00066 13.92 2.038e-10 488-501 PD00066 13.92 8.615e-10 645-658 PD00066 13.92 6.700e-09 757-770

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1068	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.950e-13 388-405 BL00028 16.07 6.400e-13 444-461 BL00028 16.07 1.692e-11 227-244 BL00028 16.07 3.423e-11 332-349 BL00028 16.07 6.538e-11 685-702 BL00028 16.07 7.231e-11 713-730 BL00028 16.07 7.577e-11 573-590 BL00028 16.07 4.300e-10 601-618 BL00028 16.07 5.500e-10 171-188 BL00028 16.07 5.800e-10 255-272 BL00028 16.07 7.900e-10 657-674 BL00028 16.07 9.700e-10 526-543 BL00028 16.07 2.029e-09 283-300 BL00028 16.07 3.829e-09 741-758 BL00028 16.07 6.914e-09 360-377 BL00028 16.07 7.686e-09 416-433
1068	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.750e-14 570-584 PR00048A 10.52 2.929e-13 329-343 PR00048A 10.52 5.500e-13 224-238 PR00048A 10.52 1.000e-12 598-612 PR00048A 10.52 5.235e-12 252-266 PR00048A 10.52 5.765e-12 441-455 PR00048A 10.52 7.353e-12 385-399 PR00048A 10.52 7.353e-12 413-427 PR00048A 10.52 7.353e-12 710-724 PR00048A 10.52 3.842e-11 357-371 PR00048A 10.52 5.263e-11 626-640 PR00048A 10.52 5.737e-11 280-294 PR00048A 10.52 7.632e-11 682-696 PR00048A 10.52 8.579e-11 654-668 PR00048B 6.02 2.125e-10 457-467 PR00048A 10.52 2.565e-10 738-752 PR00048A 10.52 6.087e-10 523-537 PR00048B 6.02 7.188e-10 698-708 PR00048B 6.02 7.750e-10 726-736 PR00048B 6.02 1.000e-09 240-250 PR00048A 10.52 3.520e-09 308-322 PR00048A 10.52 4.600e-09 551-565 PR00048A 10.52 8.560e-09 196-210 PR00048B 6.02 1.000e-08 586-596
1069	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 1.545e-11 117-158
1070	PF00168	C2 domain proteins.	PF00168C 27.49 1.750e-09 202-228
1070	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 2.227e-09 219-233
1075	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962D 10.40 3.054e-10 178-202
1075	PR00320	G-PROTEIN BETA WD-40 REPEAT	PR00320A 16.74 2.976e-09 181-

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		SIGNATURE	196
1078	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 2.478e-13 310-323
1078	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09 41-52
1078	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.931e-11 214-229 PR00320B 12.19 3.829e-10 214-229 PR00320C 13.01 3.880e-10 214-229 PR00320C 13.01 4.900e-09 257-272
1079	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subunit).	PF00774D 10.59 8.396e-09 339-365
1079	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.839e-09 588-632
1080	BL00615	C-type lectin domain proteins.	BL00615A 16.68 3.160e-11 129-147
1081	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.705e-11 47-86
1082	BL00359	Ribosomal protein L11 proteins.	BL00359B 23.07 7.462e-24 160-201 BL00359C 22.18 6.586e-22 215-249 BL00359A 20.66 4.000e-21 124-160
1082	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 1.000e-08 144-177
1084	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 1.220e-09 104-139
1084	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.000e-17 755-772 BL00028 16.07 6.625e-15 699-716 BL00028 16.07 8.412e-14 223-240 BL00028 16.07 8.941e-14 167-184 BL00028 16.07 6.850e-13 391-408 BL00028 16.07 1.783e-12 559-576 BL00028 16.07 2.957e-12 307-324 BL00028 16.07 7.652e-12 503-520 BL00028 16.07 7.652e-12 811-828 BL00028 16.07 8.043e-12 335-352 BL00028 16.07 1.346e-11 447-464 BL00028 16.07 2.385e-11 867-884 BL00028 16.07 4.462e-11 671-688 BL00028 16.07 5.846e-11 587-604 BL00028 16.07 6.192e-11 839-856 BL00028 16.07 6.192e-11 895-912 BL00028 16.07 8.962e-11 531-548 BL00028 16.07 1.600e-10 279-296 BL00028 16.07 1.600e-10 363-380 BL00028 16.07 6.100e-10 111-128 BL00028 16.07 6.700e-10 643-660 BL00028 16.07 8.500e-10 251-268 BL00028 16.07 1.771e-09 783-800 BL00028 16.07 5.886e-09 475-492
1084	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.600e-18 696-710 PR00048A 10.52 5.091e-15 164-178 PR00048A 10.52 6.727e-15 836-850 PR00048A 10.52



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			1.000e-14 220-234 PR00048A 10.52 2.500e-14 444-458 PR00048A 10.52 5.500e-14 556-570 PR00048A 10.52 9.250e-14 388-402 PR00048A 10.52 1.643e-13 640-654 PR00048A 10.52 3.571e-13 304-318 PR00048A 10.52 3.571e-13 528-542 PR00048A 10.52 8.071e-13 332-346 PR00048A 10.52 8.071e-13 808-822 PR00048A 10.52 8.071e-13 864-878 PR00048A 10.52 8.714e-13 500-514 PR00048A 10.52 7.353e-12 892-906 PR00048B 6.02 1.000e-11 292-302 PR00048B 6.02 1.000e-11 516-526 PR00048B 6.02 1.000e-11 824-834 PR00048A 10.52 3.842e-11 276-290 PR00048A 10.52 6.684e-11 584-598 PR00048A 10.52 9.053e-11 668-682 PR00048A 10.52 4.130e-10 360-374 PR00048A 10.52 6.870e-10 752-766 PR00048B 6.02 1.474e-09 768-778 PR00048B 6.02 3.368e-09 236-246 PR00048B 6.02 3.368e-09 460-470 PR00048B 6.02 4.789e-09 152-162 PR00048B 6.02 4.789e-09 376-386 PR00048B 6.02 4.789e-09 600-610 PR00048A 10.52 4.960e-09 108-122 PR00048A 10.52 4.960e-09 248-262 PR00048B 6.02 6.211e-09 264-274 PR00048B 6.02 6.211e-09 488-498 PR00048B 6.02 6.211e-09 796-806 PR00048B 6.02 7.632e-09 404-414 PR00048B 6.02 7.632e-09 712-722 PR00048A 10.52 8.920e-09 780-794
1084	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.600e-14 295-308 PD00066 13.92 1.600e-14 323-336 PD00066 13.92 1.600e-14 519-532 PD00066 13.92 1.600e-14 547-560 PD00066 13.92 1.600e-14 827-840 PD00066 13.92 1.600e-14 855-868 PD00066 13.92 5.200e-14 351-364 PD00066 13.92 5.200e-14 575-588 PD00066 13.92 8.200e-14 883-896 PD00066 13.92 9.400e-14 239-252 PD00066 13.92 2.500e-13 155-168 PD00066 13.92 2.500e-13 379-392 PD00066 13.92 2.286e-12 267-280 PD00066 13.92 2.286e-12 491-504 PD00066

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			13.92 2.286e-12 799-812 PD000066 13.92 2.714e-12 463-476 PD000066 13.92 2.714e-12 715-728 PD000066 13.92 2.714e-12 771-784 PD000066 13.92 3.571e-12 687-700 PD000066 13.92 7.000e-12 407-420 PD000066 13.92 1.000e-10 127-140 PD000066 13.92 1.000e-08 603-616
1085	PR00679	PROHIBITIN SIGNATURE	PR00679F 8.03 6.478e-28 178-202 PR00679C 14.44 7.677e-22 107-126 PR00679E 12.82 5.171e-19 153-173 PR00679D 11.91 9.053e-18 130-147 PR00679G 6.13 7.882e-17 201-218 PR00679B 13.63 2.444e-10 84-104
1086	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245E 12.40 8.286e-12 45-60
1086	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 5.814e-09 26-53
1087	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 6.885e-10 99-120
1088	BL01145	Ribosomal protein L34e proteins.	BL01145A 13.73 1.000e-12 3-45
1093	BL00154	E1-E2 ATPases phosphorylation site proteins.	BL00154D 12.57 7.387e-09 95-106
1093	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE	PR00121E 13.97 9.444e-09 92-111
1095	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e-15 439-452 PD00066 13.92 2.800e-14 411-424 PD00066 13.92 2.800e-14 467-480 PD00066 13.92 5.800e-14 495-508 PD00066 13.92 5.800e-14 523-536 PD00066 13.92 8.200e-14 355-368 PD00066 13.92 5.500e-13 579-592 PD00066 13.92 3.143e-12 551-564 PD00066 13.92 4.857e-12 383-396
1095	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.150e-13 367-384 BL00028 16.07 8.200e-13 563-580 BL00028 16.07 3.348e-12 479-496 BL00028 16.07 7.652e-12 423-440 BL00028 16.07 8.826e-12 619-636 BL00028 16.07 4.115e-11 451-468 BL00028 16.07 5.500e-11 395-412 BL00028 16.07 7.231e-11 591-608 BL00028 16.07 1.600e-10 339-356 BL00028 16.07 2.200e-10 535-552
1095	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.375e-16 560-574 PR00048A 10.52 4.214e-13 476-490 PR00048A 10.52 6.143e-13 364-378 PR00048B 6.02 6.400e-13 492-502 PR00048B 6.02 1.000e-11 352-362 PR00048B 6.02 1.000e-11 408-

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			418 PR00048B 8.02 1.692e-11 548-558 PR00048A 10.52 1.947e-11 588-602 PR00048A 10.52 3.842e-11 420-431 PR00048B 6.02 4.462e-11 462-474 PR00048A 10.52 2.684e-11 392-406 PR00048A 10.52 6.684e-11 448-462 PR00048B 6.02 7.231e-11 436-446 PR00048A 10.52 5.696e-10 532-546 PR00048B 6.02 5.263e-09 576-586 PR00048A 10.52 6.400e-09 504-518 PR00048A 10.52 6.760e-09 336-350 PR00048A 10.52 7.120e-09 616-630
1095	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 9.232e-09 472-507
1097	BL00649	G-protein coupled receptors family 2 proteins.	BL00649C 17.82 9.542e-12 400-426
1097	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249C 17.08 8.839e-11 402-426 PR00249A 15.88 7.851e-09 330-355
1097	PR00248	METABOTROPIC GLUTAMATE GPCR SIGNATURE	PR00248E 17.85 9.366e-09 442-465
1100	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 8.875e-09 886-902
1101	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.655e-16 255-273 PR00205A 14.73 1.000e-12 180-196 PR00205B 11.39 4.927e-10 475-493 PR00205C 13.65 9.438e-10 515-530
1101	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 1.000e-40 148-196 BL00232A 27.72 5.125e-25 54-87 BL00232B 32.79 4.286e-19 257-305 BL00232C 10.65 7.429e-16 255-273 BL00232B 32.79 1.500e-10 372-420 BL00232C 10.65 6.538e-10 475-493 BL00232C 10.65 7.632e-09 146-164
1103	BL00122	Carboxylesterases type-B serine proteins.	BL00122A 12.04 3.152e-15 86-107 BL00122D 12.53 7.097e-14 197-213 BL00122B 16.84 1.346e-13 148-159 BL00122C 7.91 9.550e-10 168-179
1105	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 217-230 BL00018 7.41 8.650e-10 133-146
1105	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450E 12.14 3.438e-15 174-193 PR00450B 11.76 5.574e-13 82-102 PR00450D 16.58 6.714e-13 152-172 PR00450C 12.22 6.864e-12 128-150 PR00450G 15.33 6.591e-09 224-245
1108	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.143e-12 927-940 PD00066 13.92 7.000e-09 343-356
1108	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.250e-13 911-928 BL00028 16.07 9.100e-13

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			327-344 BL00028 16.07 3.348e-12 939-956 BL00028 16.07 5.500e-11 270-287 BL00028 16.07 4.000e-10 298-315 BL00028 16.07 6.700e-10 968-985 BL00028 16.07 9.700e-10 191-208 BL00028 16.07 9.700e-10 355-372 BL00028 16.07 4.857e-09 384-401 BL00028 16.07 7.171e-09 242-259
1108	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 6.000e-12 924-934 PR00048A 10.52 4.522e-10 324-338 PR00048A 10.52 4.913e-10 908-922 PR00048A 10.52 7.652e-10 936-950 PR00048A 10.52 4.600e-09 965-979 PR00048A 10.52 7.480e-09 352-366
1108	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 9.100e-09 910-917
1109	DM01857	5 kw NUCLEOSIDE TRANSPORT DEPENDENT NA.	DM01857B 14.94 6.471e-19 284-312 DM01857E 18.90 7.313e-18 488-527 DM01857F 12.86 7.045e-15 548-575 DM01857C 15.62 4.500e-14 312-344 DM01857A 20.25 1.667e-13 207-250 DM01857D 16.80 3.165e-12 372-410
1112	DM01840	kw SPAC24B11.09 R07E5.13.	DM01840B 22.04 1.844e-40 59-103 DM01840A 10.95 9.571e-13 31-43
1114	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e-14 53-97
1114	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 9.308e-16 53-75 PR00449C 17.27 8.920e-15 94-117 PR00449B 14.34 5.680e-10 76-93
1114	PR00879	FISH ACETYLCHOLINESTERASE SIGNATURE	PR00879A 6.28 1.450e-09 37-43
1114	BL01125	ROK family proteins.	BL01125D 13.61 7.429e-09 214-227
1115	PF00622	Domain in SP1a and the RYanodine Receptor.	PF00622B 21.00 2.500e-13 265-287
1115	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 9.571e-10 103-112
1116	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 5.050e-11 66-80 PR00019B 11.36 6.850e-10 63-77
1116	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315G 15.85 6.362e-10 84-120 DM00315G 15.85 3.340e-09 246-282
1117	BL00509	Ras GTPase-activating proteins.	BL00509B 10.28 5.263e-10 429-440
1117	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.357e-10 794-809 PR00049D 0.00 1.915e-09 793-808 PR00049D 0.00 3.593e-09 792-807 PR00049D 0.00 5.729e-09 791-806
1117	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 7.559e-09 780-813

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1117	PR00806	VINCULIN SIGNATURE	PR00806A 6.63 8.397e-09 794-805
1120	PR00720	MAMMALIAN LMW PHOSPHOTYROSINE PROTEIN PHOSPHATASE SIGNATURE	PR00720C 12.41 1.099e-27 88-109 PR00720B 10.61 4.789e-20 71-87 PR00720A 16.54 2.000e-17 28-41 PR00720E 10.01 1.342e-16 117-139 PR00720D 17.32 1.778e-15 110-127
1120	PR00719	LMW PHOSPHOTYROSINE PROTEIN PHOSPHATASE SIGNATURE	PR00719A 14.49 3.000e-23 9-27 PR00719C 14.10 5.000e-18 85-101 PR00719B 14.32 1.346e-15 52-69 PR00719D 17.52 9.654e-15 110-124
1121	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 7.987e-09 108-162
1123	BL00615	C-type lectin domain proteins.	BL00615A 16.68 9.526e-13 573-591
1123	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356C 13.33 3.793e-10 591-609 PR00356D 13.09 5.038e-09 619-636
1123	PR00439	11-S SEED STORAGE PROTEIN FAMILY SIGNATURE	PR00439C 15.32 9.217e-09 332-353
1127	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 5.781e-15 493-510 BL00134B 15.99 4.194e-14 675-699
1127	BL00021	Kringle domain proteins.	BL00021B 13.33 8.984e-12 493-511
1127	BL00495	Apple domain proteins.	BL00495N 11.04 9.735e-11 667-702
1127	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 5.345e-14 251-269 PR00453B 14.65 4.682e-10 290-305
1127	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 9.129e-13 494-510 PR00722C 10.87 4.273e-11 674-687 PR00722B 12.51 4.000e-09 554-569
1127	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 5.348e-09 674-688
1128	BL00236	Neurotransmitter-gated ion-channels proteins.	BL00236D 25.66 4.000e-30 64-106
1128	PR00252	NEUROTRANSMITTER-GATED ION CHANNEL FAMILY SIGNATURE	PR00252D 12.29 7.097e-10 71-84
1129	BL00604	Synaptophysin / synaptoporin proteins.	BL00604F 5.96 7.718e-10 367-412
1129	PR00524	CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE	PR00524F 5.36 7.415e-09 208-222
1129	BL01113	CIq domain proteins.	BL01113A 17.99 6.455e-14 158-185 BL01113A 17.99 5.622e-13 28-55 BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 4.462e-12 230-257 BL01113A 17.99 6.538e-12 34-61 BL01113A 17.99 1.000e-11 284-311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e-11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A 17.99 6.523e-11 456-483

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			BL01113A 17.99 7.341e-11 411-438 BL01113A 17.99 1.766e-10 402-429 BL01113A 17.99 2.915e-10 356-383 BL01113A 17.99 6.745e-10 239-266 BL01113A 17.99 7.319e-10 293-320 BL01113A 17.99 8.085e-10 164-191 BL01113A 17.99 8.660e-10 305-332 BL01113A 17.99 2.038e-09 272-299 BL01113A 17.99 2.212e-09 353-380 BL01113A 17.99 2.385e-09 86-113 BL01113A 17.99 2.731e-09 149-176 BL01113A 17.99 2.904e-09 453-480 BL01113A 17.99 3.423e-09 131-158 BL01113A 17.99 3.423e-09 308-335 BL01113A 17.99 3.769e-09 396-423 BL01113A 17.99 3.769e-09 450-477 BL01113A 17.99 3.942e-09 25-52 BL01113A 17.99 3.942e-09 173-200 BL01113A 17.99 4.115e-09 278-305 BL01113A 17.99 4.981e-09 43-70 BL01113A 17.99 5.327e-09 19-46 BL01113A 17.99 5.500e-09 320-347 BL01113A 17.99 6.192e-09 143-170 BL01113A 17.99 7.231e-09 224-251 BL01113A 17.99 8.269e-09 245-272
1129	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 3.571e-13 31-60 BL00420A 20.42 9.082e-13 113-142 BL00420A 20.42 8.691e-11 311-340 BL00420A 20.42 4.098e-10 125-154 BL00420A 20.42 4.541e-10 158-187 BL00420A 20.42 5.279e-10 34-63 BL00420A 20.42 5.426e-10 137-166 BL00420A 20.42 6.754e-10 49-78 BL00420A 20.42 6.902e-10 266-295 BL00420A 20.42 7.492e-10 43-72 BL00420A 20.42 8.082e-10 25-54 BL00420A 20.42 9.852e-10 167-196 BL00420A 20.42 2.800e-09 170-199 BL00420A 20.42 2.938e-09 414-443 BL00420A 20.42 3.492e-09 52-81 BL00420A 20.42 5.015e-09 305-334 BL00420A 20.42 5.569e-09 37-66 BL00420A 20.42 7.923e-09 459-488 BL00420A 20.42 8.477e-09 335-364 BL00420A 20.42 8.754e-09 83-112 BL00420A 20.42 9.446e-09 287-316 BL00420A 20.42 9.862e-09 290-319

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1132	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE	PR00042E 9.69 7.652e-09 234-258
1135	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.400e-14 365-378 PD00066 13.92 6.143e-12 335-348 PD00066 13.92 2.174e-11 395-408
1135	BL00970	Nuclear transition protein 2 proteins.	BL00970B 10.09 3.069e-10 55-81
1135	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.746e-09 223-238 PR00049D 0.00 3.746e-09 224-239 PR00049D 0.00 3.898e-09 220-235
1135	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.885e-11 349-366 BL00028 16.07 5.886e-09 379-396
1135	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 6.211e-09 362-372
1135	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.169e-09 221-254
1136	BL00962	Ribosomal protein S2 proteins.	BL00962D 22.51 5.500e-35 131-175 BL00962C 15.90 9.591e-17 106-124 BL00962B 36.15 9.060e-15 40-94
1136	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE	PR00395C 16.17 1.000e-17 106-124 PR00395D 13.04 7.000e-17 131-149 PR00395F 10.56 6.400e-16 169-184 PR00395E 14.46 4.103e-11 148-160
1137	BL00152	ATP synthase alpha and beta subunits proteins.	BL00152A 15.38 5.109e-14 128-154
1139	BL00152	ATP synthase alpha and beta subunits proteins.	BL00152B 21.40 4.273e-37 124-162 BL00152A 15.38 8.364e-23 67-93
1139	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 2.862e-09 139-161
1140	BL00152	ATP synthase alpha and beta subunits proteins.	BL00152B 21.40 2.000e-32 185-223 BL00152A 15.38 8.364e-23 128-154
1140	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.672e-09 200-222
1141	PR00493	BREAST CANCER TYPE I SUSCEPTIBILITY PROTEIN SIGNATURE	PR00493G 7.57 1.184e-10 652-673
1141	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 3.700e-10 494-507
1141	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 3.667e-09 102-111
1141	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.047e-15 501-556 PF00791B 28.49 9.386e-14 468-523 PF00791C 20.98 9.814e-10 515-554 PF00791C 20.98 7.618e-09 482-521
1141	PF00023	Ank repeat proteins.	PF00023A 16.03 3.500e-12 534-550 PF00023A 16.03 7.857e-11 501-517 PF00023B 14.20 9.591e-09 497-507
1143	BL00301	GTP-binding elongation factors proteins.	BL00301A 12.41 1.750e-12 72-84
1143	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE	PR00315A 11.81 4.000e-14 72-86 PR00315B 11.66 7.600e-10 118-

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			127
1145	BL00745	Prokaryotic-type class I peptide chain release factors signal.	BL00745C 13.66 7.398e-18 59-106
1146	BL00745	Prokaryotic-type class I peptide chain release factors signal.	BL00745C 13.66 4.706e-12 59-106
1149	BL00660	Band 4.1 family domain proteins.	BL00660B 17.33 4.800e-27 136-176 BL00660A 31.50 7.911e-20 52-105 BL00660C 23.36 2.241e-19 215-259 BL00660E 23.41 9.647e-13 301-324
1149	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 4.300e-17 154-175 PR00935D 10.20 1.281e-14 215-232 PR00935B 10.58 6.108e-12 141-155 PR00935A 10.16 3.605e-10 76-89
1149	PR00661	ERM FAMILY SIGNATURE	PR00661C 9.53 3.616e-10 150-172
1153	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 1.882e-12 155-174
1153	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 1.818e-15 155-186 BL00107B 13.31 8.714e-11 221-237
1153	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 1.774e-09 90-138
1153	BL00240	Receptor tyrosine kinase class III proteins.	BL00240E 11.56 6.657e-09 141-179
1153	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 9.000e-09 200-213
1155	PR00837	ALLERGEN VS/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 4.064e-11 155-172 PR00837A 14.77 4.960e-10 78-97 PR00837B 11.64 1.310e-09 133-147
1155	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 8.759e-12 156-177 BL01009C 10.54 1.730e-09 133-147
1155	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199F 16.19 9.483e-09 113-140
1156	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 8.909e-13 4-48
1156	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 2.059e-19 4-26 PR00449C 17.27 1.000e-18 44-67 PR00449B 14.34 6.727e-11 27-44
1159	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175D 27.67 4.000e-40 367-419 BL00175C 23.75 6.870e-28 316-348 BL00175A 15.42 8.200e-19 252-272 BL00175B 12.60 8.714e-17 299-312
1159	BL00300	SRP54-type proteins GTP-binding domain proteins.	BL00300B 20.56 7.554e-11 38-84
1160	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-14 547-560 PD00066 13.92 2.200e-14 353-366 PD00066 13.92 3.400e-14 241-254 PD00066 13.92 6.400e-14 325-338 PD00066 13.92 1.500e-13 297-310 PD00066 13.92 6.500e-13 465-478 PD00066 13.92 7.500e-13 437-450 PD00066 13.92 8.500e-13 409-422 PD00066 13.92



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			2.714e-12 269-282 PD00066 13.92 3.571e-12 381-394 PD00066 13.92 7.577e-10 519-532
1160	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.647e-14 531-548 BL00028 16.07 9.471e-14 309-326 BL00028 16.07 1.900e-13 559-576 BL00028 16.07 7.750e-13 477-494 BL00028 16.07 2.174e-12 337-354 BL00028 16.07 6.478e-12 225-242 BL00028 16.07 8.043e-12 421-438 BL00028 16.07 9.217e-12 365-382 BL00028 16.07 2.038e-11 253-270 BL00028 16.07 7.231e-11 281-298 BL00028 16.07 6.100e-10 449-466 BL00028 16.07 8.800e-10 503-520 BL00028 16.07 5.371e-09 393-410
1160	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.429e-13 418-432 PR00048A 10.52 2.588e-12 362-376 PR00048A 10.52 3.647e-12 556-570 PR00048A 10.52 8.412e-12 474-488 PR00048A 10.52 9.471e-12 222-236 PR00048A 10.52 2.421e-11 306-320 PR00048B 6.02 4.462e-11 350-360 PR00048A 10.52 5.737e-11 250-264 PR00048A 10.52 7.632e-11 528-542 PR00048A 10.52 8.579e-11 278-292 PR00048A 10.52 9.053e-11 446-460 PR00048B 6.02 9.308e-11 544-554 PR00048B 6.02 9.308e-11 572-582 PR00048B 6.02 1.000e-10 406-416 PR00048A 10.52 2.565e-10 334-348 PR00048B 6.02 4.938e-10 378-388 PR00048A 10.52 5.304e-10 390-404 PR00048B 6.02 8.313e-10 238-248 PR00048B 6.02 1.947e-09 434-444 PR00048B 6.02 2.421e-09 462-472 PR00048B 6.02 3.368e-09 322-332 PR00048B 6.02 3.842e-09 266-276 PR00048B 6.02 6.211e-09 294-304
1161	PD02331	CYCLIN CELL CYCLE DIVISION PROTE.	PD02331C 13.84 1.913e-11 9-36
1161	BL00048	Protamine P1 proteins.	BL00048 6.39 3.700e-09 165-192 BL00048 6.39 4.938e-09 281-308
1161	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 9.328e-11 169-189 DM01206B 10.69 1.247e-10 248-268 DM01206B 10.69 7.781e-10 200-220 DM01206B 10.69 6.582e-09 246-266
1163	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 3.915e-15 100-148

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1163	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 6.362e-13 165-184
1163	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 1.000e-10 208-221
1163	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-26 165-196 BL00107B 13.31 3.647e-09 230-246
1164	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.135e-22 501-545 BL01013A 25.14 4.600e-14 220-256 BL01013C 9.97 4.906e-12 330-340 BL01013B 11.33 3.017e-11 287-298
1167	BL00289	Pentaxin family proteins.	BL00289A 30.36 6.850e-26 25-56 BL00289E 18.00 6.684e-14 78-93
1167	PR00895	PENTAXIN SIGNATURE	PR00895A 14.53 1.563e-15 48-63 PR00895G 14.55 5.846e-12 75-87
1167	PR00468	PLANT LIPOXYGENASE SIGNATURE	PR00468I 13.42 9.870e-09 59-74
1168	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 7.527e-09 547-563
1169	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756D 10.58 1.529e-21 367-383 PR00756B 14.06 5.737e-16 253-269 PR00756A 12.90 1.237e-13 205-221 PR00756E 11.91 4.094e-13 386-399 PR00756C 11.60 6.108e-11 331-342
1169	BL00142	Neutral zinc metalloproteases, zinc-binding region proteins.	BL00142 8.38 5.500e-10 367-378
1170	DM01688	2 POLY-IG RECEPTOR.	DM01688I 14.97 6.279e-09 75-123
1172	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 2.523e-10 40-50 PR00308C 3.83 8.892e-10 41-51 PR00308C 3.83 8.892e-10 42-52 PR00308B 4.28 6.671e-09 40-52
1172	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 7.115e-09 30-45
1179	BL00300	SRP54-type proteins GTP-binding domain proteins.	BL00300C 25.57 6.000e-09 215-269
1180	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 9.463e-19 233-270 BL00514E 14.28 7.750e-12 293-310 BL00514D 15.35 9.824e-11 274-287 BL00514G 15.98 4.273e-10 356-386 BL00514H 14.95 6.217e-09 391-416
1181	BL01158	Macrophage migration inhibitory factor family proteins.	BL01158A 21.81 4.130e-30 2-47 BL01158B 17.07 4.316e-29 47-74
1182	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 6.250e-40 46-101 BL00456C 24.55 6.586e-40 184-239 BL00456B 18.94 8.125e-25 122-152 BL00456D 6.92 5.500e-10 476-486
1185	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 4.780e-14 241-261
1185	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 1.976e-10 231-252 PR00918A 13.76 2.084e-10 495-516
1185	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-	PR00300A 9.56 5.857e-12 237-

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		BINDING SUBUNIT SIGNATURE	256 PR00300A 9.56 5.909e-09 501-520
1185	BL00370	PEP-utilizing enzymes phosphorylation site proteins proteins.	BL00370A 5.71 6.294e-09 79-87
1185	BL00113	Adenylate kinase proteins.	BL00113A 12.74 7.231e-09 502-519
1185	BL00674	AAA-protein family proteins.	BL00674D 23.41 2.286e-30 324-371 BL00674B 4.46 1.205e-17 234-256 BL00674C 22.60 2.059e-17 531-574 BL00674B 4.46 4.886e-17 498-520 BL00674E 15.24 2.800e-15 402-422 BL00674C 22.60 7.600e-09 270-313
1185	BL00870	Chaperonins clpA/B proteins.	BL00870A 11.78 9.534e-09 210-257
1185	BL00675	Sigma-54 interaction domain proteins ATP-binding region A proteins.	BL00675A 24.86 9.775e-09 237-281
1186	PR00165	ANION EXCHANGER SIGNATURE	PR00165I 10.02 8.412e-14 829-849 PR00165A 9.84 6.423e-13 495-518 PR00165B 15.26 9.090e-11 520-541 PR00165F 10.39 6.663e-10 639-658
1186	BL00291	Prion protein.	BL00291A 4.49 9.675e-10 436-471
1186	BL00219	Anion exchangers family proteins.	BL00219B 14.47 2.707e-24 296-340 BL00219C 17.29 5.426e-23 341-380 BL00219K 12.73 9.100e-23 831-873 BL00219M 9.98 9.299e-23 916-962 BL00219H 10.06 5.705e-21 618-666 BL00219I 6.16 4.968e-20 741-795 BL00219A 17.13 7.833e-19 122-154 BL00219E 11.63 2.988e-16 485-525 BL00219F 10.52 8.953e-14 525-549 BL00219G 12.86 8.163e-13 578-617 BL00219L 18.71 8.423e-13 873-912 BL00219N 10.66 6.942e-12 978-1022 BL00219D 15.15 5.286e-11 380-416 BL00219O 14.02 3.377e-09 1023-1063
1186	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 7.833e-09 452-467
1186	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 4.296e-10 446-466 DM01724 8.14 6.447e-09 442-462 DM01724 8.14 7.987e-09 438-458
1187	BL00027	'Homeobox' domain proteins.	BL00027 26.43 7.943e-14 65-108
1187	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 4.000e-11 51-67
1187	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 7.660e-10 54-93
1187	PR00028	POU DOMAIN SIGNATURE	PR00028D 17.92 2.286e-09 49-70
1189	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 2.047e-10 469-518
1192	BL01215	Mrp family proteins.	BL01215A 9.75 2.436e-09 466-493
1192	BL00567	Phosphoribulokinase proteins.	BL00567A 10.66 5.757e-09 470-

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			489
1192	PR00364	DISEASE RESISTANCE PROTEIN SIGNATURE	PR00364A 8.19 7.341e-09 470-486
1192	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.062e-09 472-489
1193	PR00303	PREPROTEIN TRANSLOCASE SECY SUBUNIT SIGNATURE	PR00303G 10.45 8.759e-09 88-111
1197	PF00429	ENV polypeptide (coat polypeptide).	PF00429 31.08 8.015e-16 415-465
1198	BL00415	Synapsins proteins.	BL00415N 4.29 7.115e-10 224-268
1198	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 1.307e-09 253-265
1198	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 7.537e-12 245-266 PR00211B 0.86 2.644e-10 251-272 PR00211B 0.86 4.083e-09 233-254 PR00211B 0.86 7.583e-09 239-260
1198	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.688e-12 227-260 DM00215 19.43 6.250e-12 225-258 DM00215 19.43 5.235e-11 232-265 DM00215 19.43 5.941e-11 242-275 DM00215 19.43 4.375e-10 236-269 DM00215 19.43 4.857e-10 222-255 DM00215 19.43 5.179e-10 230-263 DM00215 19.43 8.554e-10 237-270 DM00215 19.43 2.068e-09 215-248 DM00215 19.43 3.898e-09 235-268 DM00215 19.43 4.508e-09 240-273 DM00215 19.43 5.576e-09 231-264 DM00215 19.43 6.339e-09 220-253 DM00215 19.43 9.847e-09 218-251
1200	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 4.326e-22 81-129
1202	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.214e-16 108-148 BL00237C 13.19 3.323e-11 245-272 BL00237B 5.28 2.227e-09 182-194
1202	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 4.600e-13 250-275 PR00237E 13.03 1.000e-12 174-198 PR00237G 19.63 7.469e-12 288-315 PR00237B 13.50 7.207e-11 75-97 PR00237C 15.69 7.750e-09 122-145
1203	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.214e-16 108-148 BL00237C 13.19 3.323e-11 280-307 BL00237B 5.28 2.227e-09 217-229
1203	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 4.600e-13 285-310 PR00237E 13.03 1.000e-12 209-233 PR00237G 19.63 7.469e-12 323-350 PR00237B 13.50 7.207e-11 75-97 PR00237C 15.69 7.750e-09 122-145
1207	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259B 14.81 3.769e-21 50-77 PR00259C 16.40 4.000e-20 77-106 PR00259A 9.27 3.600e-16

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			12-36
1207	BL00421	Transmembrane 4 family proteins	BL00421B 17.62 7.261e-36 56-95 BL00421A 11.79 8.313e-16 8-27
1207	PR00164	ABC-2 TYPE TRANSPORT SYSTEM MEMBRANE PROTEIN SIGNATURE	PR00164D 13.90 1.486e-09 9-34
1208	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.207e-14 562-585
1208	BL00216	Sugar transport proteins.	BL00216B 27.64 3.250e-10 267-317
1209	PF00922	Vesiculovirus phosphoprotein.	PF00922A 19.17 7.724e-09 88-122
1214	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.143e-10 17-32
1214	PD01351	PROTEIN REPEAT NEUROFILAMENT TRIPL.	PD01351B 13.72 9.518e-10 18-44 PD01351B 13.72 3.758e-09 24-50
1214	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.576e-09 5-38
1214	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 7.857e-09 17-30
1215	BL00612	Osteonectin domain proteins.	BL00612E 13.12 3.947e-11 379-424
1215	BL00484	Thyroglobulin type-1 repeat proteins proteins.	BL00484C 17.01 3.854e-11 131-146 BL00484B 9.04 1.491e-10 238-252 BL00484C 17.01 8.560e-10 258-273 BL00484B 9.04 3.850e-09 111-125
1216	BL00223	Annexins repeat proteins domain proteins.	BL00223A 15.59 1.000e-33 147-181 BL00223A 15.59 1.435e-16 75-109 BL00223C 24.79 3.928e-15 134-189
1216	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196C 10.36 3.571e-25 151-173 PR00196A 11.16 7.300e-24 84-107 PR00196B 10.68 4.808e-16 124-141 PR00196A 11.16 6.236e-14 156-179 PR00196E 9.19 1.000e-12 155-176 PR00196G 11.72 5.829e-11 199-213 PR00196C 10.36 7.913e-11 79-101
1216	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201D 10.49 8.729e-14 151-173 PR00201A 6.05 1.976e-13 84-107 PR00201G 11.02 3.847e-12 155-182 PR00201A 6.05 8.241e-12 156-179 PR00201H 12.04 4.889e-10 199-213
1216	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198D 7.65 7.787e-21 151-173 PR00198B 8.71 3.880e-17 84-107 PR00198C 14.32 2.688e-11 124-141 PR00198G 8.09 7.033e-10 155-176
1216	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200E 10.00 5.030e-19 151-173 PR00200G 9.43 5.546e-14 155-182 PR00200B 7.39 4.653e-11 156-179 PR00200B 7.39 4.857e-10 84-107 PR00200H 13.68 9.663e-10 199-213
1216	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202D 5.58 6.793e-14 151-173 PR00202G 8.01 5.545e-13 155-182 PR00202B 11.44 2.782e-10 155-179 PR00202B 11.44

SEQ ID NO:	Database entry ID	Description	Results*
1216	PR00197	ANNEXIN TYPE I SIGNATURE	5.206e-09 83-107 PR00197B 7.56 4.960e-29 84-107 PR00197D 7.50 3.000e-26 151-173 PR00197A 8.68 7.577e-20 35-51 PR00197C 7.50 1.000e-19 124-141 PR00197F 9.03 7.128e-10 155-176 PR00197D 7.50 6.250e-09 79-101
1216	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199D 5.65 9.297e-17 151-173 PR00199B 6.86 2.915e-13 84-107 PR00199B 6.86 1.265e-11 156-179 PR00199G 9.09 4.351e-11 156-182 PR00199D 5.65 3.641e-09 79-101 PR00199C 13.84 9.571e-09 124-141
1217	BL00223	Annexins repeat proteins domain proteins.	BL00223B 28.47 1.000e-40 188-238 BL00223A 15.59 1.000e-33 119-153 BL00223A 15.59 1.435e-16 47-81 BL00223C 24.79 3.928e-15 106-161
1217	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201D 10.49 8.729e-14 123-145 PR00201A 6.05 1.976e-13 56-79 PR00201G 11.02 3.847e-12 127-154 PR00201A 6.05 8.241e-12 128-151 PR00201E 12.37 3.317e-11 206-233 PR00201H 12.04 4.889e-10 171-185
1217	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198D 7.65 7.787e-21 123-145 PR00198B 8.71 3.880e-17 56-79 PR00198E 14.67 5.286e-15 206-233 PR00198C 14.32 2.688e-11 96-113 PR00198G 8.09 7.033e-10 127-148
1217	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196D 21.86 1.000e-27 206-233 PR00196C 10.36 3.571e-25 123-145 PR00196A 11.16 7.300e-24 56-79 PR00196B 10.68 4.808e-16 96-113 PR00196A 11.16 6.236e-14 128-151 PR00196E 9.19 1.000e-12 127-148 PR00196G 11.72 5.829e-11 171-185 PR00196C 10.36 7.913e-11 51-73 PR00196C 10.36 8.750e-10 282-304
1217	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202D 5.58 6.793e-14 123-145 PR00202G 8.01 5.545e-13 127-154 PR00202E 13.00 8.740e-11 206-233 PR00202B 11.44 2.782e-10 127-151 PR00202B 11.44 5.206e-09 55-79
1217	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197E 11.89 1.794e-32 206-233 PR00197B 7.56 4.960e-29 56-79 PR00197D 7.50 3.000e-26 123-145 PR00197A 8.68 7.577e-20 7-23 PR00197C 7.50 1.000e-19 96-113 PR00197F 9.03 7.128e-10 127-148 PR00197D 7.50 6.250e-09 51-73

SEQ ID NO:	Database entry ID	Description	Results*
1217	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200E 10.00 5.030e-19 123-145 PR00200G 9.43 5.546e-14 127-154 PR00200B 7.39 4.653e-11 128-151 PR00200F 13.72 7.094e-11 206-233 PR00200B 7.39 4.857e-10 56-79 PR00200H 13.68 9.663e-10 171-185 PR00200E 10.00 8.842e-09 282-304
1217	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199D 5.65 9.297e-17 123-145 PR00199F 16.19 4.391e-15 206-233 PR00199B 6.86 2.915e-13 56-79 PR00199B 6.86 1.265e-11 128-151 PR00199G 9.09 4.351e-11 128-154 PR00199D 5.65 3.641e-09 51-73 PR00199C 13.84 9.571e-09 96-113
1218	BL00223	Annexins repeat proteins domain proteins.	BL00223A 15.59 1.000e-33 119-153 BL00223A 15.59 1.435e-16 47-81 BL00223C 24.79 3.928e-15 106-161
1218	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196C 10.36 3.571e-25 123-145 PR00196A 11.16 7.300e-24 56-79 PR00196B 10.68 4.808e-16 96-113 PR00196A 11.16 6.236e-14 128-151 PR00196E 9.19 1.000e-12 127-148 PR00196G 11.72 5.829e-11 171-185 PR00196C 10.36 7.913e-11 51-73
1218	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201D 10.49 8.729e-14 123-145 PR00201A 6.05 1.976e-13 56-79 PR00201G 11.02 3.847e-12 127-154 PR00201A 6.05 8.241e-12 128-151 PR00201H 12.04 4.889e-10 171-185
1218	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198D 7.65 7.787e-21 123-145 PR00198B 8.71 3.880e-17 56-79 PR00198C 14.32 2.688e-11 96-113 PR00198G 8.09 7.033e-10 127-148
1218	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200E 10.00 5.030e-19 123-145 PR00200G 9.43 5.546e-14 127-154 PR00200B 7.39 4.653e-11 128-151 PR00200B 7.39 4.857e-10 56-79 PR00200H 13.68 9.663e-10 171-185
1218	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202D 5.58 6.793e-14 123-145 PR00202G 8.01 5.545e-13 127-154 PR00202B 11.44 2.782e-10 127-151 PR00202B 11.44 5.206e-09 55-79
1218	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197B 7.56 4.960e-29 56-79 PR00197D 7.50 3.000e-26 123-145 PR00197A 8.68 7.577e-20 7-23 PR00197C 7.50 1.000e-19 96-113 PR00197F 9.03 7.128e-10 127-148 PR00197D 7.50 6.250e-09 51-73

SEQ ID NO:	Database entry ID	Description	Results*
1218	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199D 5.65 9.297e-17 123-145 PR00199B 6.86 2.915e-13 56-79 PR00199B 6.86 1.265e-11 128-151 PR00199G 9.09 4.351e-11 128-154 PR00199D 5.65 3.641e-09 51-73 PR00199C 13.84 9.571e-09 96-113
1221	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.	BL00086 20.87 8.615e-27 423-455
1221	PR00465	E-CLASS P450 GROUP IV SIGNATURE	PR00465F 13.37 8.468e-12 393-412
1221	PR00359	B-CLASS P450 SIGNATURE	PR00359I 11.13 7.261e-11 433-445
1221	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463I 15.02 9.571e-21 433-457 PR00463G 18.24 6.760e-19 388-413 PR00463E 17.37 6.595e-17 304-331 PR00463F 17.63 7.568e-12 347-366 PR00463B 17.50 7.692e-12 79-101 PR00463D 14.02 8.875e-11 284-302 PR00463C 12.85 6.932e-10 171-190
1221	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464G 12.41 2.588e-12 398-414 PR00464E 18.28 3.077e-10 342-363 PR00464I 14.64 3.106e-10 433-457 PR00464H 13.32 4.635e-09 420-434 PR00464D 17.40 5.787e-09 313-331 PR00464C 18.84 5.808e-09 284-313
1221	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385E 12.66 9.100e-14 433-445 PR00385A 14.97 5.696e-13 295-313 PR00385B 10.22 6.400e-09 313-327
1221	PR00408	MITOCHONDRIAL P450 SIGNATURE	PR00408D 15.44 6.831e-09 295-313
1222	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385A 14.97 5.696e-13 295-313
1222	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463B 17.50 7.692e-12 79-101 PR00463D 14.02 8.875e-11 284-302 PR00463C 12.85 6.932e-10 171-190
1222	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464C 18.84 5.808e-09 284-313
1222	PR00408	MITOCHONDRIAL P450 SIGNATURE	PR00408D 15.44 6.831e-09 295-313
1223	BL00477	Alpha-2-macroglobulin family thiolester region proteins.	BL00477A 13.50 9.182e-19 70-99
1225	BL00500	Thymosin beta-4 family proteins.	BL00500 9.77 2.565e-28 2-42
1227	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.971e-10 231-246 PR00320C 13.01 8.200e-10 231-246 PR00320B 12.19 9.486e-10 231-246 PR00320B 12.19 3.475e-09 188-203 PR00320B 12.19 4.600e-09 315-330 PR00320C 13.01 4.900e-09 315-330
1227	PR00319	BETA G-PROTEIN (TRANSDUCIN)	PR00319B 11.47 9.143e-09 315-



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		SIGNATURE	330
1227	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.600e-10 233-244 BL00678 9.67 1.000e-08 317-328
1236	PF00580	UvrD/REP helicase.	PF00580D 13.15 8.920e-13 670-684 PF00580E 13.89 2.800e-11 867-886 PF00580F 8.62 9.438e-10 913-926
1237	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.000e-09 64-78 PR00019A 11.19 8.000e-09 90-104
1238	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e-10 229-250
1243	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 4.759e-09 464-484
1243	BL00315	Dehydrins proteins.	BL00315A 9.35 1.000e-08 389-417
1245	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.054e-15 191-209
1246	PF00023	Ank repeat proteins.	PF00023A 16.03 9.500e-12 347-363 PF00023A 16.03 8.500e-10 283-299 PF00023A 16.03 8.875e-10 184-200
1246	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 1.989e-13 217-272 PF00791B 28.49 6.044e-13 117-172 PF00791B 28.49 4.316e-12 184-239 PF00791B 28.49 9.432e-12 250-305 PF00791B 28.49 6.243e-10 84-139 PF00791C 20.98 4.971e-09 98-137
1246	BL00906	Uroporphyrinogen decarboxylase proteins.	BL00906D 24.33 7.750e-09 212-256
1248	BL00415	Synapsins proteins.	BL00415Q 2.23 8.297e-09 13-49
1250	BL01113	C1q domain proteins.	BL01113B 18.26 2.500e-13 841-877
1252	BL01248	Laminin-type EGF-like (LE) domain proteins.	BL01248 11.02 7.171e-12 258-271 BL01248 11.02 7.943e-12 325-338
1252	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 7.000e-17 376-395 PR00011A 14.06 1.000e-14 376-395 PR00011B 13.08 5.167e-14 376-395 PR00011C 24.25 8.468e-14 395-424 PR00011D 14.03 9.739e-09 249-268
1253	BL00164	Enolase proteins.	BL00164A 11.58 2.800e-28 41-64
1253	PR00148	ENOLASE SIGNATURE	PR00148A 10.11 1.783e-18 44-59
1255	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 8.322e-14 102-128 BL01153C 13.67 6.507e-10 51-65
1256	BL00892	HIT family proteins.	BL00892B 16.86 1.000e-20 130-154 BL00892A 18.17 6.657e-20 64-95
1256	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE	PR00332B 13.62 3.000e-16 76-95 PR00332C 7.37 4.600e-14 143-154 PR00332A 10.15 7.375e-12 55-72
1257	PF00791	Domain present in ZO-1 and Unc5-like netrin	PF00791B 28.49 4.146e-10 73-

SEQ ID NO:	Database entry ID	Description	Results*
		receptors.	128
1258	BL00615	C-type lectin domain proteins.	BL00615B 12.25 5.200e-12 166-180
1259	BL00071	Glyceraldehyde 3-phosphate dehydrogenase proteins.	BL00071B 21.70 1.000e-40 80-126 BL00071C 11.81 1.000e-40 146-181 BL00071D 19.39 3.118e-25 184-239 BL00071E 11.48 4.600e-24 308-329 BL00071A 5.81 2.607e-14 5-17
1259	PR00078	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00078B 7.45 3.250e-24 146-165 PR00078D 11.49 2.800e-21 231-249 PR00078E 10.50 6.211e-16 271-287 PR00078A 10.38 1.000e-15 111-125 PR00078C 15.99 6.211e-11 173-190
1262	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 2.688e-10 15-38 PR00926D 10.53 6.625e-10 21-40
1262	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 6.143e-10 44-66 PR00927B 14.66 9.870e-10 265-287 PR00927A 14.66 5.685e-09 46-68
1262	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 6.250e-17 13-38 BL00215A 15.82 1.600e-15 230-255 BL00215A 15.82 5.974e-13 108-133 BL00215B 10.44 7.600e-09 275-288
1263	PR00654	ANGIOTENSINOGEN SIGNATURE	PR00654A 15.64 1.540e-26 23-44 PR00654D 10.48 3.538e-26 153-175 PR00654F 15.16 8.071e-26 255-275 PR00654E 9.81 2.241e-25 194-215 PR00654C 9.50 5.500e-21 115-135
1263	BL00284	Serpins proteins.	BL00284C 28.56 9.514e-21 254-296 BL00284E 19.15 9.710e-16 439-464 BL00284A 15.64 8.147e-14 113-137 BL00284D 16.34 1.837e-12 361-388 BL00284B 17.99 7.500e-11 229-250
1264	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.071e-17 34-57
1265	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.600e-16 34-57
1266	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 2.800e-16 31-54
1267	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 9.400e-16 34-57
1268	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 4.000e-21 282-300 BL00290A 20.89 4.600e-16 34-57 BL00290A 20.89 2.421e-13 225-248
1269	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.600e-16 34-57
1271	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.071e-17 34-57
1272	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.600e-16 34-57
1273	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.600e-16 34-57

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		histocompatibility complex proteins.	
1274	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 2.500e-14 46-59
1274	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 6.063e-09 300-310
1274	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 7.750e-11 472-486 PR00501A 8.25 7.955e-09 328-342
1281	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 3.919e-15 101-119 BL00972B 9.45 7.577e-10 180-190
1285	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 5.941e-09 213-234
1286	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 5.941e-09 259-280
1287	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 3.000e-19 19-39 PR00625B 13.48 2.756e-17 47-68
1287	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 7.600e-19 23-40 BL00636B 15.11 6.870e-15 47-68
1288	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.714e-10 24-33
1289	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500I 9.22 1.107e-31 2810-2833 PR00500G 3.68 1.087e-30 2525-2548 PR00500H 17.80 1.107e-29 2662-2684 PR00500E 6.99 1.106e-27 2350-2370 PR00500F 9.44 1.108e-26 2483-2503
1289	PF00801	PKD domain proteins.	PF00801B 23.63 9.217e-26 1055-1083 PF00801A 13.49 6.276e-11 222-235 PF00801B 23.63 3.087e-10 719-747 PF00801B 23.63 6.609e-10 1652-1680
1291	BL00415	Synapsins proteins.	BL00415N 4.29 5.401e-09 136-180
1292	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 2.800e-23 229-270 PD00930A 25.62 5.021e-12 125-151
1292	PF00620	GTPase-activator protein for Rho-like GTPases.	PF00620B 14.20 7.000e-12 178-195
1293	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.043e-34 281-318 BL00023 24.31 5.320e-32 223-260 BL00023 24.31 5.800e-29 340-377
1293	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 1.000e-12 398-409
1293	PR00138	MATRIXIN SIGNATURE	PR00138D 16.56 5.500e-30 398-424 PR00138C 16.41 1.000e-29 164-193 PR00138B 15.82 5.875e-16 141-157 PR00138A 15.14 1.000e-15 94-108 PR00138E 6.01 8.472e-11 431-445
1293	BL00024	Hemopexin domain proteins.	BL00024C 22.98 1.000e-40 163-212 BL00024D 17.28 4.316e-36 392-424 BL00024B 21.53 7.545e-33 115-149 BL00024F 11.30 2.895e-18 486-507 BL00024A 11.49 3.667e-12 94-105

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			BL00024G 13.31 4.857e-12 525-538 BL00024E 7.58 2.263e-10 431-445
1293	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 1.771e-09 393-412
1293	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE	PR00013C 12.29 7.136e-19 372-388 PR00013C 12.29 6.464e-18 313-329 PR00013C 12.29 5.500e-16 255-271 PR00013B 14.75 4.375e-12 355-368 PR00013A 12.26 1.973e-11 344-354 PR00013A 12.26 6.595e-11 227-237 PR00013B 14.75 8.568e-10 296-309 PR00013A 12.26 2.167e-09 285-295 PR00013B 14.75 2.588e-09 238-251
1293	BL00546	Matrixins cysteine switch.	BL00546B 20.11 3.368e-40 164-208 BL00546C 16.41 6.400e-31 392-424 BL00546A 19.62 6.523e-19 74-104 BL00546E 10.23 7.947e-13 486-507 BL00546F 12.40 5.339e-09 525-538
1294	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.043e-34 281-318 BL00023 24.31 5.320e-32 223-260 BL00023 24.31 5.800e-29 340-377
1294	BL00546	Matrixins cysteine switch.	BL00546B 20.11 3.368e-40 164-208 BL00546C 16.41 6.400e-31 392-424 BL00546A 19.62 6.523e-19 74-104
1294	PR00138	MATRIXIN SIGNATURE	PR00138D 16.56 5.500e-30 398-424 PR00138C 16.41 1.000e-29 164-193 PR00138B 15.82 5.875e-16 141-157 PR00138A 15.14 1.000e-15 94-108
1294	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.	BL00142 8.38 1.000e-12 398-409
1294	BL00024	Hemopexin domain proteins.	BL00024C 22.98 1.000e-40 163-212 BL00024D 17.28 4.316e-36 392-424 BL00024B 21.53 7.545e-33 115-149 BL00024A 11.49 3.667e-12 94-105
1294	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 1.771e-09 393-412
1294	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE	PR00013C 12.29 7.136e-19 372-388 PR00013C 12.29 6.464e-18 313-329 PR00013C 12.29 5.500e-16 255-271 PR00013B 14.75 4.375e-12 355-368 PR00013A 12.26 1.973e-11 344-354 PR00013A 12.26 6.595e-11 227-237 PR00013B 14.75 8.568e-10 296-309 PR00013A 12.26 2.167e-09 285-295 PR00013B 14.75 2.588e-09 238-251
1298	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354R 8.50 2.969e-22 2115-2145 DM01354S 11.61 1.692e-14

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			2145-2166
1298	DM01688	2 POLY-IG RECEPTOR.	DM01688E 13.44 8.244e-09 1714-1737
1298	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.737e-10 1807-1817 DM00179 13.97 7.158e-10 1077-1087 DM00179 13.97 9.053e-10 759-769 DM00179 13.97 9.053e-10 1328-1338 DM00179 13.97 4.130e-09 574-584 DM00179 13.97 4.130e-09 1431-1441 DM00179 13.97 6.870e-09 1713-1723 DM00179 13.97 7.652e-09 850-860 DM00179 13.97 8.435e-09 2089-2099
1298	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.909e-13 623-647 BL00240B 24.70 1.209e-10 1126-1150 BL00240B 24.70 4.558e-10 124-148 BL00240B 24.70 6.442e-10 529-553 BL00240B 24.70 4.255e-09 1222-1246 BL00240B 24.70 8.468e-09 995-1019
1298	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 8.091e-09 1126-1148 PD02327B 19.84 9.318e-09 1222-1244
1298	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 1.200e-10 1610-1643 PD02870B 18.83 7.400e-10 2081-2114 PD02870B 18.83 7.800e-10 1069-1102 PD02870B 18.83 5.213e-09 1423-1456 PD02870B 18.83 6.649e-09 67-100 PD02870B 18.83 7.989e-09 1518-1551 PD02870D 15.74 8.564e-09 566-601 PD02870B 18.83 9.521e-09 286-319 PD02870B 18.83 9.904e-09 1258-1291
1299	BL00888	Cyclic nucleotide-binding domain proteins.	BL00888B 14.79 4.706e-18 372-396 BL00888A 18.03 1.000e-08 354-371
1301	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 9.625e-16 73-90 PF00615C 10.06 9.206e-12 150-164
1302	BL00766	Tetrahydrofolate dehydrogenase/cyclohydrolase proteins.	BL00766E 13.78 9.625e-39 191-228 BL00766C 25.86 4.375e-31 77-125 BL00766D 17.05 5.966e-25 152-182
1302	PR00085	TETRAHYDROFOLATE DEHYDROGENASE/CYCLOHYDROLASE FAMILY SIGNATURE	PR00085E 15.79 7.000e-26 151-181 PR00085G 10.74 1.865e-22 208-227 PR00085C 15.23 6.182e-21 47-69 PR00085D 15.02 2.688e-20 92-113 PR00085F 9.77 6.595e-15 191-208
1303	BL00180	Glutamine synthetase proteins.	BL00180E 17.60 1.000e-40 154-206 BL00180D 13.26 2.174e-24 119-141 BL00180F 10.05 6.211e-17 218-231 BL00180G 10.20

SEQ ID NO:	Database entry ID	Description	Results*
			8.435e-17 307-322 BL00180C 12.14 4.600e-14 102-112 BL00180B 18.03 4.971e-14 68-87 BL00180A 13.20 5.065e-14 32-45
1304	BL00180	Glutamine synthetase proteins.	BL00180F 10.05 6.750e-15 49-62
1306	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 1.000e-08 77-123
1308	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191A 8.16 5.440e-09 36-49
1309	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191A 8.16 5.440e-09 61-74
1310	PF00606	Herpesviral Glycoprotein B.	PF00606I 20.74 7.894e-09 264-316
1310	BL01219	Ammonium transporters proteins.	BL01219D 11.63 2.957e-10 217-241 BL01219F 15.24 8.809e-09 335-360
1310	PR00342	RHESUS BLOOD GROUP PROTEIN SIGNATURE	PR00342G 8.18 1.458e-19 220-239 PR00342B 11.09 8.657e-13 61-79 PR00342D 8.46 2.857e-12 128-145 PR00342I 4.99 6.016e-12 285-299 PR00342H 7.61 6.927e-11 250-273 PR00342C 10.10 4.770e-10 90-108 PR00342E 14.49 5.950e-10 151-175 PR00342F 7.02 1.556e-09 185-201 PR00342J 8.97 7.940e-09 308-327 PR00342L 7.61 9.600e-09 398-424
1311	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 9.080e-11 80-99 PR00209B 4.88 6.967e-10 86-105
1311	DM00406	GLIADIN.	DM00406 7.73 1.400e-09 86-99
1311	PR00501	KELCH REPEAT SIGNATURE	PR00501B 18.88 8.342e-09 440-455
1312	PR00528	GLUCOCORTICOID RECEPTOR SIGNATURE	PR00528F 9.13 9.063e-09 31-51
1313	PF00622	Domain in SPla and the Ryanodine Receptor.	PF00622C 12.62 6.625e-13 759-773
1313	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39 BL00518 12.23 1.667e-09 356-365
1314	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 2.824e-25 37-92 BL00420C 11.90 9.250e-12 122-133
1314	PR00258	SPERACT RECEPTOR SIGNATURE	PR00258D 14.41 6.333e-11 98-113 PR00258B 9.63 7.474e-11 52-64 PR00258E 13.33 1.750e-09 121-134 PR00258C 9.05 5.167e-09 67-78
1315	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 8.548e-10 122-134
1315	BL00766	Tetrahydrofolate dehydrogenase/cyclohydrolase proteins.	BL00766C 25.86 7.632e-09 20-68
1315	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 2.452e-13 41-59 PR00081C 15.13 9.229e-09 167-184
1317	BL00263	Natriuretic peptides proteins.	BL00263 11.87 5.909e-22 129-147

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1317	PR00711	ATRIAL NATRIURETIC PEPTIDE SIGNATURE	PR00711G 11.75 1.113e-30 128-151 PR00711B 10.71 7.545e-24 32-51 PR00711D 7.91 1.000e-22 72-90 PR00711F 3.17 2.463e-22 109-128 PR00711C 5.66 7.818e-22 51-70 PR00711E 6.39 1.000e-21 92-109 PR00711A 12.00 9.769e-20 11-30
1317	PR00713	C-TYPE NATRIURETIC PEPTIDE SIGNATURE	PR00713C 14.14 1.370e-13 130-146
1317	PR00710	NATRIURETIC PEPTIDE FAMILY SIGNATURE	PR00710A 10.90 3.250e-14 127-137 PR00710B 11.08 1.391e-12 136-146
1317	PR00712	BRAIN NATRIURETIC PEPTIDE SIGNATURE	PR00712D 10.52 4.109e-12 128-139 PR00712E 10.62 7.231e-10 138-152
1318	BL00609	Glycosyl hydrolases family 32 proteins.	BL00609C 13.27 9.270e-11 249-261
1318	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 6.538e-16 757-773 BL01187B 12.04 7.750e-14 610-626 BL01187B 12.04 8.200e-14 651-667 BL01187B 12.04 2.029e-10 523-539 BL01187A 9.98 7.429e-10 591-603
1318	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 6.301e-11 753-770 PR00907B 11.29 2.636e-10 647-664 PR00907B 11.29 3.524e-09 519-536 PR00907G 11.63 4.243e-09 651-678
1318	BL01177	Anaphylatoxin domain proteins.	BL01177C 17.39 8.286e-09 517-536
1318	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 1.429e-09 762-773 PR00010C 11.16 8.500e-09 528-539
1318	BL00022	EGF-like domain proteins.	BL00022B 7.54 1.000e-08 619-626
1319	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 4.000e-10 26-50
1320	BL00125	Serine/threonine specific protein phosphatases proteins.	BL00125D 33.11 9.719e-35 23-78
1320	PR00114	SERINE/THREONINE PHOSPHATASE FAMILY SIGNATURE	PR00114F 17.51 4.706e-16 39-60 PR00114G 17.20 5.421e-12 61-78
1321	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.	BL00453B 23.86 6.538e-26 281-315 BL00453A 15.57 8.364e-12 249-264 BL00453C 9.72 3.250e-11 323-336
1321	PR00280	CHANNEL FORMING COLICIN SIGNATURE	PR00280A 11.09 8.227e-09 284-300
1322	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 8.261e-09 310-328
1322	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 9.500e-09 45-59
1323	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 8.269e-16 34-56
1323	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 2.474e-09 34-78
1323	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 6.260e-09 36-55

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1323	BL00567	Phosphoribulokinase proteins.	BL00567A 10.66 9.100e-09 35-54
1324	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.847e-10 314-333
1324	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242G 13.52 6.276e-09 748-788
1324	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 381-397 BL00107A 18.39 8.091e-09 314-345
1325	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.847e-10 314-333
1325	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242G 13.52 6.276e-09 721-761
1325	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 381-397 BL00107A 18.39 8.091e-09 314-345
1326	BL00472	Small cytokines (intercrine/chemokine) C-C subfamily signature.	BL00472C 20.76 8.225e-09 50-87
1327	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 8.667e-13 114-130 PR00705B 10.22 2.385e-10 293-304
1327	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 8.125e-17 312-329 BL00139C 9.23 2.800e-10 292-302 BL00139B 10.19 7.600e-10 157-166 BL00139A 10.29 2.723e-09 114-124
1328	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 8.667e-13 155-171 PR00705B 10.22 2.385e-10 334-345
1328	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 8.125e-17 353-370 BL00139C 9.23 2.800e-10 333-343 BL00139B 10.19 7.600e-10 198-207 BL00139A 10.29 2.723e-09 155-165
1330	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 7.443e-10 129-169 PD01270A 17.22 7.387e-09 36-76
1332	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.772e-10 250-301
1332	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.068e-09 751-784
1333	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 8.594e-35 151-199 BL00232B 32.79 5.579e-22 260-308 BL00232A 27.72 1.000e-20 57-90 BL00232C 10.65 3.613e-14 258-276 BL00232B 32.79 4.872e-11 377-425 BL00232C 10.65 3.211e-09 480-498
1333	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 9.113e-10 698-718 DM01724 8.14 6.803e-09 694-714
1333	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 4.545e-15 258-276 PR00205A 14.73 5.600e-09 183-199 PR00205B 11.39 8.017e-09 480-498
1335	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 9.000e-29 47-92 BL00214A 21.17 1.000e-24 6-32
1335	PR00178	FATTY ACID-BINDING PROTEIN	PR00178C 20.54 3.864e-25 65-93



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		SIGNATURE	PR00178A 15.07 7.188e-23 7-28 PR00178D 13.52 6.170e-12 111-130
1336	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 8.250e-09 509-525
1338	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.759e-17 112-130 BL00972D 22.55 8.116e-12 354-379 BL00972B 9.45 7.088e-09 193-203
1340	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 3.155e-09 1-44
1340	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633E 12.18 4.682e-10 182-199 PR00633G 13.71 1.667e-09 185-204 PR00633H 15.10 3.963e-09 244-266
1340	BL00625	Regulator of chromosome condensation (RCC1) proteins.	BL00625B 17.69 5.219e-15 179-213 BL00625B 17.69 9.194e-14 343-377 BL00625A 16.21 4.405e-12 185-214 BL00625A 16.21 5.500e-12 129-158 BL00625A 16.21 7.203e-12 349-378 BL00625B 17.69 5.778e-10 123-157 BL00625B 17.69 5.034e-09 285-319
1342	BL00476	Fatty acid desaturases family 1 proteins.	BL00476F 12.75 6.551e-09 45-90
1345	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.690e-11 292-307 PR00320B 12.19 4.343e-10 292-307 PR00320C 13.01 7.840e-10 292-307
1345	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.000e-09 294-305
1345	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.	BL00225B 18.06 7.273e-22 6-41 BL00225B 18.06 5.673e-14 97-132 BL00225A 13.82 7.218e-09 61-82
1350	PD01823	PROTEIN INTERGENIC REGION ABC1 PRECURSOR MITOCHONDRION T.	PD01823D 16.66 3.093e-15 21-42 PD01823E 9.30 5.909e-15 75-88
1352	BL00540	Ferritin iron-binding regions proteins.	BL00540A 15.06 1.000e-40 9-50 BL00540B 18.82 1.000e-40 100-155 BL00540C 13.00 7.500e-15 165-177
1353	PR00294	STREPTOMYCES SUBTILISIN INHIBITOR SIGNATURE	PR00294A 10.44 6.444e-10 159-186
1353	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 7.167e-10 206-245
1356	BL00428	Cell cycle proteins fisW / rodA / spoVE proteins.	BL00428A 14.30 3.613e-09 91-110
1359	BL00142	Neutral zinc metalloproteases, zinc-binding region proteins.	BL00142 8.38 7.188e-10 389-400
1359	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 7.983e-16 550-578 PD01719B 9.30 1.750e-09 877-885 PD01719A 12.89 3.000e-09 1006-1034
1359	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 3.186e-09 384-403
1360	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 6.330e-11 232-271 DM00191D 13.94 7.728e-11 48-87 DM00191D 13.94 5.000e-10 112-151 DM00191D 13.94

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			5.667e-10 59-98 DM00191D 13.94 5.667e-10 123-162 DM00191D 13.94 6.583e-10 56-95 DM00191D 13.94 8.417e-10 280-319 DM00191D 13.94 8.917e-10 192-231 DM00191D 13.94 1.391e-09 224-263 DM00191D 13.94 2.409e-09 208-247 DM00191D 13.94 4.835e-09 120-159 DM00191D 13.94 5.304e-09 149-188 DM00191D 13.94 5.461e-09 211-250 DM00191D 13.94 6.322e-09 80-119 DM00191D 13.94 7.652e-09 243-282 DM00191D 13.94 8.513e-09 216-255 DM00191D 13.94 9.452e-09 177-216
1360	PF00624	Flocculin repeat proteins.	PF00624J 6.21 3.496e-11 237-292 PF00624J 6.21 6.597e-11 53-108 PF00624J 6.21 4.121e-10 253-308 PF00624J 6.21 5.718e-10 141-196 PF00624F 11.04 1.508e-09 50-86 PF00624J 6.21 3.163e-09 101-156 PF00624J 6.21 3.233e-09 165-220 PF00624I 9.10 5.181e-09 140-170 PF00624F 11.04 6.008e-09 130-166 PF00624J 6.21 6.093e-09 125-180 PF00624J 6.21 6.163e-09 221-276 PF00624G 10.91 6.806e-09 45-100 PF00624G 10.91 7.169e-09 181-236 PF00624G 10.91 7.387e-09 221-276 PF00624J 6.21 8.674e-09 197-252 PF00624J 6.21 8.884e-09 117-172 PF00624J 6.21 8.884e-09 213-268 PF00624J 6.21 9.512e-09 55-110
1360	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 6.163e-10 22-71 BL00115Z 3.12 7.618e-09 36-85 BL00115Z 3.12 9.603e-09 241-290
1363	PF00023	Ank repeat proteins.	PF00023A 16.03 1.321e-09 110-126
1363	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.527e-13 110-165 PF00791B 28.49 6.119e-09 77-132 PF00791C 20.98 7.529e-09 91-130
1366	PF00168	C2 domain proteins.	PF00168C 27.49 9.250e-17 320-346
1366	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399A 9.52 1.844e-14 148-164 PR00399C 12.82 8.071e-14 218-234 PR00399B 14.27 2.853e-13 163-177 PR00399D 14.48 1.871e-11 238-249
1366	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.759e-12 337-351 PR00360A 14.59 3.903e-10 308-321 PR00360B 13.61 4.789e-10 203-217

SEQ ID NO:	Database entry ID	Description	Results*
1367	PF00168	C2 domain proteins.	PF00168C 27.49 9.250e-17 320-346
1367	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399A 9.52 1.844e-14 148-164 PR00399C 12.82 8.071e-14 218-234 PR00399B 14.27 2.853e-13 163-177 PR00399D 14.48 1.871e-11 238-249
1367	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.759e-12 337-351 PR00360A 14.59 3.903e-10 308-321 PR00360B 13.61 4.789e-10 203-217
1368	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.	BL00086 20.87 1.857e-20 444-476
1368	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464I 14.64 4.375e-17 454-478 PR00464A 20.47 9.591e-16 130-151 PR00464C 18.84 1.000e-15 305-334 PR00464D 17.40 6.250e-15 334-352 PR00464H 13.32 8.941e-15 441-455 PR00464F 15.23 9.654e-13 403-419 PR00464B 20.41 1.844e-12 186-205 PR00464E 18.28 7.907e-12 363-384 PR00464G 12.41 8.412e-12 419-435
1368	PR00465	E-CLASS P450 GROUP IV SIGNATURE	PR00465H 17.76 6.586e-10 454-473
1368	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385A 14.97 1.346e-12 316-334 PR00385B 10.22 4.130e-11 334-348 PR00385D 13.11 7.857e-10 445-455 PR00385E 12.66 9.438e-10 454-466
1368	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463G 18.24 3.605e-14 409-434 PR00463E 17.37 4.814e-11 325-352 PR00463I 15.02 5.574e-09 454-478 PR00463H 12.41 7.158e-09 444-455
1370	BL00218	Amino acid permeases proteins.	BL00218D 21.49 9.757e-11 263-308
1371	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.288e-09 35-50
1372	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 84-106 PR00380C 13.18 5.286e-17 240-259 PR00380D 9.93 7.698e-17 290-312 PR00380B 12.64 7.805e-14 207-225
1372	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 7.750e-25 241-283 BL00411C 15.04 2.500e-22 84-106 BL00411H 15.66 8.235e-16 289-320 BL00411E 10.43 9.129e-16 135-154 BL00411F 14.77 9.795e-16 198-223 BL00411D 12.13 5.909e-09 114-125
1373	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 1.915e-09 590-605
1373	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 5.800e-12 158-172 PR00019B 11.36 1.000e-10 130-144 PR00019A 11.19 8.826e-10 133-147 PR00019B 11.36

SEQ ID NO:	Database entry ID	Description	Results*
1373	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	7.120e-09 106-120 PR00500B 7.74 7.821e-09 250-271
1374	BL00411	Kinesin motor domain proteins.	BL00411H 15.66 7.811e-22 79-110 BL00411G 21.39 8.683e-22 31-73
1374	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380C 13.18 2.385e-16 30-49 PR00380D 9.93 3.739e-16 80-102
1376	BL00790	Receptor tyrosine kinase class V proteins.	BL00790E 29.58 6.667e-12 767-815
1376	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 5.636e-10 423-434 PR00010C 11.16 8.071e-09 148-159
1376	BL00022	EGF-like domain proteins.	BL00022B 7.54 8.200e-09 427-434
1376	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 7.312e-10 224-241 PR00907G 11.63 5.297e-09 62-89 PR00907B 11.29 8.354e-09 98-115 PR00907B 11.29 9.451e-09 334-351
1376	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 5.235e-15 62-78 BL01187B 12.04 5.765e-15 418-434 BL01187B 12.04 3.000e-12 143-159 BL01187B 12.04 7.333e-12 297-313 BL01187B 12.04 7.000e-11 338-354 BL01187B 12.04 4.857e-10 378-394 BL01187B 12.04 5.886e-10 102-118 BL01187A 9.98 6.571e-10 321-333 BL01187A 9.98 5.125e-09 126-138 BL01187A 9.98 9.625e-09 362-374
1377	BL00048	Protamine P1 proteins.	BL00048 6.39 4.038e-09 396-423
1381	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 8.500e-27 342-373
1381	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.412e-12 342-361
1381	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.143e-09 25-39
1382	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 6.036e-09 48-61
1388	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.261e-10 69-83 PR00019B 11.36 4.600e-09 66-80
1392	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 6.870e-09 42-55
1396	BL00790	Receptor tyrosine kinase class V proteins.	BL00790B 21.59 1.000e-40 61-113 BL00790C 16.65 1.000e-40 165-219 BL00790K 9.30 1.000e-40 657-711 BL00790Q 15.61 1.000e-40 855-904 BL00790O 7.68 5.929e-39 797-830 BL00790G 22.06 5.114e-36 376-420 BL00790R 16.20 7.469e-36 951-995 BL00790E 29.58 7.250e-35 273-321 BL00790J 14.21 8.200e-33 605-645 BL00790N 13.25 1.214e-31 763-790 BL00790I 20.01 1.931e-29 501-532 BL00790D 12.41 2.500e-27

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			243-268 BL00790H 13.42 6.478e-27 455-481 BL00790M 8.74 8.683e-25 741-763 BL00790P 12.33 3.755e-24 830-855 BL00790F 15.90 5.200e-24 339-366 BL00790L 11.16 5.909e-21 721-741 BL00790A 19.74 1.964e-19 31-53
1396	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 9.500e-16 789-837 BL00240E 11.56 1.439e-15 736-774 BL00240G 28.45 8.793e-15 836-889
1396	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.647e-20 750-781 BL00107B 13.31 5.091e-13 818-834
1396	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 9.100e-22 819-842 PR00109E 14.41 7.429e-19 863-886 PR00109B 12.27 5.125e-18 750-769 PR00109A 15.00 2.895e-13 713-727 PR00109C 12.85 5.235e-12 800-811
1396	BL00239	Receptor tyrosine kinase class II proteins.	BL00239E 17.14 5.426e-27 790-840 BL00239B 25.15 3.000e-23 684-732 BL00239F 28.15 8.132e-21 844-889 BL00239D 16.81 2.143e-10 762-788 BL00239C 18.75 3.348e-10 737-760
1396	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001B 17.40 2.714e-11 747-768 BL50001D 11.00 7.300e-10 818-829 BL50001C 10.17 1.000e-09 799-810
1396	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 8.071e-13 490-509 PR00014B 14.77 3.400e-10 467-478 PR00014D 12.04 6.824e-10 508-523 PR00014A 8.22 3.455e-09 342-352
1401	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.000e-11 84-127
1403	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.958e-09 387-441
1404	BL01113	Clq domain proteins.	BL01113B 18.26 2.500e-13 841-877
1406	BL01206	Amiloride-sensitive sodium channels proteins.	BL01206D 30.58 3.025e-28 363-412 BL01206G 21.72 6.063e-27 530-576 BL01206F 16.40 7.643e-15 485-506 BL01206E 20.72 5.650e-14 427-454 BL01206C 12.30 3.455e-12 333-352 BL01206B 13.56 1.205e-10 313-327
1408	BL01220	Phosphatidylethanolamine-binding protein family proteins.	BL01220B 16.65 1.000e-40 59-100 BL01220C 14.75 5.846e-34 100-128 BL01220A 22.62 3.400e-31 21-52
1409	BL00815	Alpha-isopropylmalate and homocitrate synthases proteins.	BL00815C 21.36 3.118e-09 786-815
1412	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.051e-09 1-16
1412	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.640e-09 3-17
1418	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.200e-09 453-

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			466
1418	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e-14 524-541 BL00028 16.07 8.269e-11 555-572 BL00028 16.07 2.543e-09 437-454 BL00028 16.07 4.600e-09 408-425 BL00028 16.07 6.657e-09 465-482
1418	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.160e-09 521-535 PR00048A 10.52 4.960e-09 434-448 PR00048A 10.52 6.760e-09 552-566 PR00048A 10.52 7.840e-09 462-476
1419	BL00022	EGF-like domain proteins.	BL00022A 7.48 5.000e-09 177-184 BL00022A 7.48 5.000e-09 241-248 BL00022A 7.48 8.000e-09 49-56
1419	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 5.696e-09 182-201 PR00011D 14.03 6.478e-09 86-105 PR00011D 14.03 9.087e-09 118-137
1419	DM01842	1 CELLULOSE-BINDING DOMAIN, BACTERIAL TYPE.	DM01842 11.31 9.922e-09 94-141
1421	PR00371	FLAVOPROTEIN PYRIDINE NUCLEOTIDE CYTOCHROME REDUCTASE SIGNATURE	PR00371D 14.55 4.536e-11 385-405
1421	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE	PR00406D 10.02 6.538e-10 385-405
1421	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 2.484e-09 385-405
1421	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466E 6.82 6.958e-17 386-404 PR00466C 10.17 8.244e-09 195-216
1422	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.462e-11 1087-1104
1422	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.478e-11 1075-1088
1422	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 4.375e-10 1154-1188
1422	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.522e-10 1084-1098 PR00048B 6.02 1.474e-09 1072-1082 PR00048A 10.52 6.760e-09 1056-1070
1423	PR00260	BACTERIAL CHEMOTAXIS SENSORY TRANSDUCER SIGNATURE	PR00260C 10.26 9.294e-09 146-167
1424	BL00845	CAP-Gly domain proteins.	BL00845 16.43 6.442e-21 405-430 BL00845 16.43 9.820e-19 203-228
1426	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.769e-15 369-382 PD00066 13.92 4.462e-15 285-298 PD00066 13.92 2.800e-14 257-270 PD00066 13.92 5.200e-14 313-326 PD00066 13.92 8.962e-10 341-354
1426	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.050e-13 269-286 BL00028 16.07 5.050e-13 297-314 BL00028 16.07 2.500e-10 325-342 BL00028 16.07 5.200e-10 353-370 BL00028

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			16.07 7.000e-10 241-258 BL00028 16.07 9.700e-10 381-398
1426	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.500e-17 266-280 PR00048A 10.52 5.500e-14 294-308 PR00048A 10.52 4.706e-12 350-364 PR00048B 6.02 6.000e-12 310-320 PR00048B 6.02 6.538e-11 394-404 PR00048A 10.52 2.565e-10 238-252 PR00048B 6.02 2.688e-10 254-264 PR00048B 6.02 4.375e-10 338-348 PR00048A 10.52 5.304e-10 378-392 PR00048A 10.52 9.609e-10 322-336 PR00048B 6.02 5.263e-09 282-292 PR00048B 6.02 6.211e-09 366-376
1429	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671C 4.18 5.345e-09 9-29
1431	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.855e-09 215-236
1431	BL00226	Intermediate filaments proteins.	BL00226D 19.10 7.400e-09 390-437
1432	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.855e-09 251-272
1432	BL00226	Intermediate filaments proteins.	BL00226D 19.10 7.400e-09 426-473
1434	PR00545	RETINOIC ACID RECEPTOR SIGNATURE	PR00545A 5.35 9.430e-09 383-398
1436	BL01238	GDA1/CD39 family of nucleoside phosphatases proteins.	BL01238A 11.72 7.840e-16 76-91
1437	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 2.800e-26 1256-1297 PD00930A 25.62 3.864e-13 1152-1178
1437	PF00620	GTPase-activator protein for Rho-like GTPases.	PF00620B 14.20 7.000e-12 1205-1222
1437	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY DOMAIN SIGNATURE	PR00683B 16.62 2.603e-10 946-968 PR00683D 15.87 2.773e-09 1005-1024
1437	PR00543	OESTROGEN RECEPTOR SIGNATURE	PR00543H 10.86 7.573e-09 556-576
1437	PF00595	PDZ domain proteins (Also known as DHR or GLGF).	PF00595 13.40 7.600e-09 90-101
1437	BL00275	Shiga/ricin ribosomal inactivating toxins proteins signatu.	BL00275A 12.16 7.677e-09 1226-1240
1441	BL00223	Annexins repeat proteins domain proteins.	BL00223B 28.47 1.000e-40 140-190 BL00223C 24.79 1.000e-40 217-272 BL00223A 15.59 5.500e-32 21-55 BL00223A 15.59 4.783e-14 230-264 BL00223C 24.79 2.515e-10 8-63 BL00223A 15.59 6.250e-10 71-105
1441	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199G 9.09 8.364e-21 239-265 PR00199F 16.19 5.636e-16 158-185 PR00199D 5.65 5.375e-14 25-47 PR00199B 6.86 1.574e-13 30-53 PR00199D 5.65 7.987e-

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			13 234-256 PR00199H 12.62 5.339e-12 282-296 PR00199D 5.65 9.276e-10 75-97
1441	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200F 13.72 1.118e-35 158-185 PR00200G 9.43 1.000e-34 238-265 PR00200B 7.39 1.643e-29 30-53 PR00200H 13.68 1.766e-18 282-296 PR00200E 10.00 6.160e-16 75-97 PR00200E 10.00 2.111e-14 25-47 PR00200A 4.93 2.125e-14 5-16 PR00200C 8.76 1.500e-12 54-63 PR00200E 10.00 2.859e-11 234-256 PR00200G 9.43 5.294e-11 29-56 PR00200D 10.01 9.722e-10 70-87
1441	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197F 9.03 5.250e-16 238-259 PR00197D 7.50 1.250e-15 25-47 PR00197E 11.89 8.463e-14 158-185 PR00197D 7.50 1.542e-12 234-256 PR00197D 7.50 5.451e-10 75-97 PR00197B 7.56 2.206e-09 30-53
1441	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198G 8.09 7.943e-16 238-259 PR00198D 7.65 2.271e-13 234-256 PR00198D 7.65 9.894e-13 25-47 PR00198E 14.67 6.381e-11 158-185 PR00198H 12.05 1.462e-10 282-296 PR00198B 8.71 9.357e-10 30-53 PR00198D 7.65 4.845e-09 75-97
1441	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201G 11.02 9.419e-26 238-265 PR00201A 6.05 4.770e-16 30-53 PR00201E 12.37 4.103e-15 158-185 PR00201H 12.04 4.375e-14 282-296 PR00201D 10.49 4.150e-10 75-97 PR00201G 11.02 8.402e-10 29-56 PR00201D 10.49 6.179e-09 25-47
1441	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301D 15.51 7.395e-09 38-59
1441	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196D 21.86 3.032e-24 158-185 PR00196E 9.19 8.333e-23 238-259 PR00196A 11.16 9.100e-21 30-53 PR00196F 13.89 2.714e-15 266-282 PR00196C 10.36 5.167e-15 25-47 PR00196G 11.72 3.000e-14 282-296 PR00196C 10.36 7.344e-13 234-256 PR00196C 10.36 1.703e-12 75-97 PR00196G 11.72 9.217e-10 207-221 PR00196F 13.89 4.188e-09 107-123 PR00196A 11.16 7.840e-09 80-103
1441	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202G 8.01 4.833e-28 238-265 PR00202E 13.00 4.643e-16 158-185 PR00202D 5.58 9.604e-13 75-97 PR00202B 11.44 2.763e-11 29-53 PR00202H 9.20



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			4.740e-11 282-296 PR00202D 5.58 1.908e-09 25-47 PR00202G 8.01 9.237e-09 29-56
1444	DM01513	CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN.	DM01513A 13.61 8.568e-14 15-56
1445	BL00603	Thymidine kinase cellular-type proteins.	BL00603C 30.02 1.000e-40 152-207 BL00603A 20.71 4.500e-33 63-96 BL00603D 10.53 5.091e-18 217-232 BL00603B 11.39 3.455e-15 132-147
1446	PD01922	PROTEIN PHOSPHODIESTERASE HYDROL.	PD01922B 21.83 7.328e-14 162-198
1447	BL00061	Short-chain dehydrogenases/reductases family proteins.	BL00061B 25.79 1.931e-13 99-137
1448	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.958e-09 64-118
1449	PF00856	SET domain proteins.	PF00856A 26.14 8.579e-11 5-42
1449	PF00628	PHD-finger.	PF00628 15.84 5.500e-10 11-26
1452	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 3.400e-10 116-126
1454	PF00075	RNase H.	PF00075D 10.71 7.000e-11 517-528 PF00075C 11.58 9.786e-11 484-496 PF00075B 12.56 4.073e-10 449-460 PF00075A 14.44 2.143e-09 402-419
1454	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 4.417e-09 138-159
1456	BL00262	Insulin family proteins.	BL00262B 16.89 8.286e-17 68-88 BL00262A 12.48 4.600e-15 32-50
1456	PR00277	INSULIN B CHAIN SIGNATURE	PR00277A 14.82 2.421e-13 29-43 PR00277B 12.79 2.350e-11 43-56
1456	PR00276	INSULIN A CHAIN SIGNATURE	PR00276A 11.84 4.750e-13 69-79 PR00276B 8.02 7.828e-10 78-88
1457	PR00213	MYELIN P0 PROTEIN SIGNATURE	PR00213E 5.51 9.775e-12 264-289
1459	BL00856	Guanylate kinase proteins.	BL00856C 29.21 2.658e-26 539-587 BL00856B 9.61 2.946e-18 511-532
1459	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 2.750e-09 369-385
1459	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.	PD00289 9.97 6.586e-09 298-312
1459	PF00595	PDZ domain proteins (Also known as DHR or GLGF).	PF00595 13.40 8.800e-09 295-306
1461	PR00475	HEXOKINASE FAMILY SIGNATURE	PR00475B 14.92 6.143e-26 186-212 PR00475E 16.08 2.742e-22 327-350 PR00475F 9.68 4.000e-20 407-430 PR00475A 14.06 3.118e-19 118-135 PR00475C 11.92 6.684e-19 239-256 PR00475G 9.08 1.692e-16 479-496 PR00475D 13.30 2.653e-13 262-277 PR00475G 9.08 2.650e-10 32-49
1461	BL00378	Hexokinases proteins.	BL00378C 16.14 1.000e-40 243-287 BL00378E 22.92 5.821e-40 313-359 BL00378B 14.23 3.647e-

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			32 98-135 BL00378F 8.27 2.688e-17 481-496 BL00378D 10.94 1.474e-13 291-303 BL00378A 19.01 8.694e-11 59-8 BL00378F 8.27 3.714e-10 34-49
1464	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 8.448e-14 56-72
1464	BL00021	Kringle domain proteins.	BL00021B 13.33 1.763e-13 55-73
1464	PR00839	V8 SERINE PROTEASE FAMILY SIGNATURE	PR00839B 11.20 4.945e-09 55-73
1464	BL01253	Type I fibronectin domain proteins.	BL01253E 16.01 6.381e-09 125-162
1464	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 3.813e-15 55-72 BL00134B 15.99 7.200e-10 186-210 BL00134C 13.45 9.206e-09 219-233
1466	BL00291	Prion protein.	BL00291A 4.49 9.379e-09 105-140
1467	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 9.581e-12 398-422
1468	PF01105	emp24/gp25L/p24 family.	PF01105B 25.12 2.868e-25 126-178
1469	PF01105	emp24/gp25L/p24 family.	PF01105B 25.12 2.868e-25 151-203
1470	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305A 9.33 9.500e-36 37-67 PR00305E 13.01 4.316e-32 177-204 PR00305D 16.34 3.647e-30 150-177 PR00305F 15.95 1.964e-26 204-234 PR00305C 8.68 3.182e-26 115-138 PR00305B 9.99 4.857e-24 84-109 PR00305F 15.95 8.975e-15 215-245
1470	BL00796	14-3-3 proteins.	BL00796C 17.44 1.000e-40 99-149 BL00796D 17.39 1.000e-40 150-196 BL00796B 10.67 7.000e-39 37-70 BL00796E 14.15 3.045e-33 198-234 BL00796A 10.52 4.656e-26 5-32 BL00796E 14.15 2.742e-11 209-245
1474	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 7.796e-10 676-687 PF00642 11.59 7.055e-09 276-287
1475	PF00588	SpoU rRNA Methylase family.	PF00588B 17.18 8.200e-10 281-303
1476	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.653e-09 791-845
1477	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.255e-14 364-385
1477	BL00306	Caseins alpha/beta proteins.	BL00306B 8.28 1.900e-09 557-568
1477	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00318E 7.23 5.320e-09 220-230
1479	BL01305	moaA / nifB / pqqE family proteins.	BL01305D 14.97 7.279e-09 7-22
1480	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 5.807e-09 458-479
1480	PR00674	LIGHT HARVESTING PROTEIN B CHAIN SIGNATURE	PR00674A 20.10 9.870e-09 133-154
1481	PR00171	SUGAR TRANSPORTER SIGNATURE	PR00171E 14.87 1.000e-08 73-86

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1482	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 5.650e-23 101-149 DM01418B 22.51 8.500e-11 166-208 DM01418C 20.48 8.655e-10 236-278
1482	BL00291	Prion protein.	BL00291A 4.49 9.349e-10 23-58
1482	BL01113	C1q domain proteins.	BL01113A 17.99 6.114e-11 38-65 BL01113A 17.99 2.915e-10 35-62 BL01113A 17.99 6.538e-09 17-44 BL01113A 17.99 6.712e-09 29-56 BL01113A 17.99 8.442e-09 32-59
1483	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 5.650e-23 117-165 DM01418B 22.51 8.500e-11 182-224 DM01418C 20.48 8.655e-10 252-294
1483	BL00291	Prion protein.	BL00291A 4.49 9.349e-10 23-58
1483	BL01113	C1q domain proteins.	BL01113A 17.99 6.114e-11 38-65 BL01113A 17.99 2.915e-10 35-62 BL01113A 17.99 6.538e-09 17-44 BL01113A 17.99 6.712e-09 29-56 BL01113A 17.99 8.442e-09 32-59
1484	BL01052	Calponin family repeat proteins.	BL01052B 15.31 3.308e-11 30-56
1484	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE	PR00888C 12.27 2.141e-09 30-46
1486	BL00795	Involucrin proteins.	BL00795C 17.06 7.600e-09 239-284
1486	BL00415	Synapsins proteins.	BL00415N 4.29 9.409e-09 818-862
1490	BL01046	ATP-dependent serine proteases, lon family, serine active sit.	BL01046D 19.61 4.938e-35 452-493 BL01046C 17.03 9.581e-31 377-421 BL01046B 19.24 4.977e-29 331-377
1490	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830D 8.08 2.552e-20 767-787 PR00830A 8.41 7.545e-18 375-395 PR00830E 13.94 8.500e-15 790-809 PR00830C 8.47 2.837e-13 737-757 PR00830B 14.73 7.429e-13 654-671
1490	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.027e-12 371-405
1490	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 1.254e-10 371-390
1490	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 2.350e-10 370-386
1490	BL00674	AAA-protein family proteins.	BL00674B 4.46 8.071e-10 368-390
1490	PR00364	DISEASE RESISTANCE PROTEIN SIGNATURE	PR00364A 8.19 1.818e-09 370-386
1490	BL00113	Adenylate kinase proteins.	BL00113A 12.74 7.369e-09 372-389
1491	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.	BL00824B 9.21 2.338e-09 150-170
1495	BL00615	C-type lectin domain proteins.	BL00615A 16.68 3.880e-11 47-65 BL00615B 12.25 2.286e-10 149-163
1498	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE	PR00119B 13.94 8.714e-12 35-50 PR00119E 8.48 7.716e-11 420-440

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1498	PR00120	H <sup>+</sup> -TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 7.037e-10 420-437
1498	BL00154	E1-E2 ATPases phosphorylation site proteins.	BL00154E 20.37 5.275e-19 263-304 BL00154F 8.23 6.175e-19 417-441 BL00154C 12.38 4.326e-13 31-50 BL00154D 12.57 5.935e-09 191-202
1499	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 3.455e-33 476-522 BL00039A 18.44 8.548e-23 145-184 BL00039C 15.63 8.500e-16 277-301 BL00039B 19.19 1.837e-12 191-217
1499	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 8.990e-12 450-497
1499	PF00271	Helicases conserved C-terminal domain proteins.	PF00271 7.99 5.500e-10 507-515
1501	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 9.669e-09 116-165
1502	PF00168	C2 domain proteins.	PF00168B 11.83 8.000e-10 38-49
1502	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 6.806e-10 43-56 PR00360B 13.61 2.227e-09 67-81 PR00360B 13.61 5.909e-09 223-237
1503	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 4.165e-13 780-835 PF00791B 28.49 6.767e-10 888-943 PF00791C 20.98 8.059e-09 794-833
1504	PF00023	Ank repeat proteins.	PF00023A 16.03 5.875e-10 437-453 PF00023A 16.03 7.000e-10 563-579 PF00023A 16.03 8.500e-10 248-264 PF00023A 16.03 9.250e-10 95-111 PF00023A 16.03 3.250e-09 596-612 PF00023A 16.03 3.893e-09 716-732 PF00023A 16.03 6.786e-09 62-78 PF00023A 16.03 9.036e-09 496-512
1504	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 2.957e-09 88-101 PD00078B 13.14 5.696e-09 556-569 PD00078B 13.14 9.217e-09 742-755
1504	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 5.024e-15 215-270 PF00791B 28.49 7.750e-14 62-117 PF00791B 28.49 9.795e-14 530-585 PF00791B 28.49 9.505e-13 683-738 PF00791B 28.49 7.253e-12 95-150 PF00791B 28.49 2.636e-11 716-771 PF00791C 20.98 5.696e-11 697-736 PF00791B 28.49 3.359e-10 404-459 PF00791B 28.49 5.369e-10 248-303 PF00791B 28.49 6.767e-10 563-618 PF00791C 20.98 8.052e-10 544-583 PF00791C 20.98 3.382e-09 229-268 PF00791B 28.49 7.275e-09 371-426 PF00791C 20.98 9.912e-09 385-424

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1505	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 8.714e-09 143-159
1506	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 8.714e-09 167-183
1507	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.286e-10 239-248
1507	BL01282	BIR repeat proteins.	BL01282B 30.49 1.900e-09 220-259
1507	BL00264	Neurohypophysial hormones proteins.	BL00264 8.98 4.884e-09 341-368
1510	BL00122	Carboxylesterases type-B serine proteins.	BL00122G 11.67 2.500e-15 15-26
1511	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 1.986e-11 340-353 PR00910A 2.51 1.986e-11 342-355 PR00910A 2.51 1.986e-11 344-357 PR00910A 2.51 9.778e-10 346-359 PR00910A 2.51 1.107e-09 338-351 PR00910A 2.51 3.464e-09 336-349
1511	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 4.508e-09 324-357
1512	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 8.475e-15 175-188
1514	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 8.375e-10 149-164 PR00833H 2.30 2.846e-09 147-162
1514	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 9.630e-11 150-165 PR00308C 3.83 8.892e-10 104-114 PR00308C 3.83 8.892e-10 105-115 PR00308C 3.83 8.892e-10 151-161 PR00308C 3.83 8.892e-10 152-162 PR00308C 3.83 8.892e-10 153-163 PR00308C 3.83 8.892e-10 154-164 PR00308C 3.83 7.545e-09 103-113 PR00308C 3.83 7.896e-09 150-160 PR00308B 4.28 8.397e-09 150-162 PR00308A 5.90 9.047e-09 101-116
1514	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.188e-10 144-159 PR00456E 3.06 1.684e-09 145-160 PR00456E 3.06 7.949e-09 97-112 PR00456E 3.06 9.430e-09 98-113
1515	PF00992	Troponin.	PF00992A 16.67 3.368e-09 448-483
1521	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.333e-09 322-336 PR00019B 11.36 9.280e-09 319-333
1522	BL00315	Dehydrins proteins.	BL00315A 9.35 7.197e-10 93-121
1524	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 4.240e-16 235-276
1524	PR00234	HIV-1 MATRIX PROTEIN SIGNATURE	PR00234E 11.78 7.268e-09 361-375
1525	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 8.338e-14 44-92
1527	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 6.850e-10 132-146 PR00019A 11.19 2.667e-09 135-149 PR00019B 11.36 9.640e-

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			09 180-194 PR00019B 11.36 1.000e-08 277-291
1529	BL00625	Regulator of chromosome condensation (RCC1) proteins.	BL00625A 16.21 2.033e-16 567-596 BL00625B 17.69 4.205e-12 561-595 BL00625B 17.69 9.423e-11 93-127 BL00625B 17.69 1.444e-10 152-186 BL00625A 16.21 1.759e-10 99-128 BL00625A 16.21 2.739e-09 515-544 BL00625B 17.69 3.172e-09 43-77 BL00625A 16.21 4.170e-09 158-187
1529	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633B 13.02 3.535e-09 561-575 PR00633A 9.32 6.260e-09 527-544 PR00633F 10.03 7.949e-09 528-543
1530	BL00414	Profilin proteins.	BL00414A 13.85 6.344e-13 2-16 BL00414E 15.46 6.283e-09 121-136
1530	PR00392	PROFILIN SIGNATURE	PR00392C 18.98 2.350e-12 41-62 PR00392A 14.10 4.176e-12 4-14 PR00392D 12.00 5.250e-11 63-78 PR00392F 17.40 7.955e-11 122-140 PR00392E 12.06 6.500e-09 109-123
1531	BL00414	Profilin proteins.	BL00414A 13.85 6.344e-13 2-16 BL00414E 15.46 6.283e-09 105-120
1531	PR00392	PROFILIN SIGNATURE	PR00392C 18.98 2.350e-12 41-62 PR00392A 14.10 4.176e-12 4-14 PR00392D 12.00 5.250e-11 63-78 PR00392F 17.40 7.955e-11 106-124 PR00392E 12.06 8.833e-09 93-107
1532	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BL.	PD00301A 10.24 8.200e-09 131-142
1533	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930F 14.16 1.310e-27 24-60
1534	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 2.200e-39 77-119 BL00411H 15.66 8.800e-33 125-156 BL00411F 14.77 6.250e-18 33-58
1534	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 7.923e-26 126-148 PR00380C 13.18 1.000e-21 76-95 PR00380B 12.64 1.621e-16 42-60
1534	BL00893	mutT domain proteins.	BL00893 18.99 8.826e-09 176-201
1536	BL00600	Aminotransferases class-III pyridoxal-phosphate attachment si.	BL00600E 16.43 5.725e-15 164-193 BL00600G 12.43 7.000e-14 242-261 BL00600F 8.77 7.480e-11 207-220 BL00600D 8.71 1.750e-10 143-157
1537	BL00838	Interleukins -4 and -13 proteins.	BL00838A 12.35 8.696e-09 136-155
1537	PD01847	PHOTOSYSTEM II PROTEIN REACTION CENTRE I TRANSM.	PD01847 9.59 8.946e-09 137-173
1539	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE	PR00121D 16.72 3.012e-12 261-283

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1539	BL00154	E1-E2 ATPases phosphorylation site proteins.	BL00154E 20.37 8.468e-16 532-573 BL00154C 12.38 3.520e-12 264-283
1539	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 6.400e-11 680-685
1539	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE	PR00119B 13.94 3.333e-11 268-283 PR00119D 9.56 6.063e-10 548-559
1540	BL00289	Pentaxin family proteins.	BL00289A 30.36 9.031e-09 331-362
1542	BL01279	Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa.	BL01279A 24.27 1.000e-11 67-115
1542	BL00422	Granins proteins.	BL00422C 16.18 7.176e-09 303-331
1545	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.462e-32 244-287
1545	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 3.143e-12 230-246
1545	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 3.500e-12 276-286 PR00024A 11.87 7.000e-12 251-263 PR00024B 11.27 1.409e-10 266-277
1545	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.414e-10 267-284
1545	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 1.675e-37 233-272 BL00032C 11.28 4.429e-21 272-290 BL00032A 18.38 5.750e-10 193-216
1546	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.400e-16 245-258 PD00066 13.92 8.615e-15 329-342 PD00066 13.92 6.000e-13 301-314 PD00066 13.92 4.857e-12 217-230 PD00066 13.92 1.346e-10 273-286 PD00066 13.92 8.200e-09 357-370
1546	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.950e-13 313-330 BL00028 16.07 7.261e-12 229-246 BL00028 16.07 3.077e-11 16-33 BL00028 16.07 3.769e-11 285-302 BL00028 16.07 9.308e-11 341-358 BL00028 16.07 3.100e-10 397-414 BL00028 16.07 5.800e-10 201-218 BL00028 16.07 6.400e-10 369-386 BL00028 16.07 7.600e-10 257-274 BL00028 16.07 8.800e-10 72-89 BL00028 16.07 9.229e-09 101-118
1546	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.118e-12 310-324 PR00048B 6.02 5.000e-12 326-336 PR00048A 10.52 6.294e-12 13-27 PR00048B 6.02 1.692e-11 242-252 PR00048A 10.52 3.842e-11 338-352 PR00048A 10.52 5.263e-11 366-380 PR00048A 10.52 8.579e-11 226-240 PR00048A 10.52 8.579e-11

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			254-268 PR00048A 10.52 3.348e-10 394-408 PR00048A 10.52 4.913e-10 282-296 PR00048B 6.02 7.188e-10 298-308 PR00048B 6.02 9.053e-09 57-67 PR00048A 10.52 9.640e-09 98-112
1547	BL00585	Ribosomal protein S5 proteins.	BL00585B 18.78 6.143e-18 303-340 BL00585A 28.43 4.286e-16 220-272
1548	PR00482	OMPTIN SERINE PROTEASE SIGNATURE	PR00482C 11.02 7.968e-09 816-842
1549	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500B 7.74 7.359e-10 56-77
1551	PR00917	SMALL ROUND STRUCTURED VIRUS (C37) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00917G 10.59 8.990e-09 812-830
1553	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.486e-09 109-126
1555	PF00638	RanBP1 domain proteins.	PF00638 11.91 4.600e-18 67-82
1555	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 1.600e-20 68-96 DM01269B 11.71 3.323e-09 138-148
1556	BL00406	Actins proteins.	BL00406E 8.44 8.541e-28 323-373 BL00406B 5.47 1.375e-27 82-137 BL00406D 12.58 3.160e-26 266-321 BL00406C 6.75 6.943e-25 141-196 BL00406A 9.95 2.575e-20 7-42
1556	PR00190	ACTIN SIGNATURE	PR00190F 7.80 3.647e-13 139-159 PR00190C 11.49 2.029e-12 60-83 PR00190G 12.62 2.050e-09 233-250
1558	BL00048	Protamine P1 proteins.	BL00048 6.39 3.700e-09 153-180
1558	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 9.328e-11 157-177 DM01206B 10.69 1.247e-10 236-256 DM01206B 10.69 7.781e-10 188-208 DM01206B 10.69 6.582e-09 234-254
1559	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE	PR00315A 11.81 5.688e-10 126-140
1559	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.000e-09 127-148
1559	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.431e-09 125-147
1559	PR00755	AFLATOXIN BIOSYNTHESIS REGULATORY PROTEIN SIGNATURE	PR00755F 10.99 9.722e-09 30-52
1563	PF00780	Domain found in NIK1-like kinases, mouse citron and yeast ROM.	PF00780B 23.03 9.908e-09 14-57
1567	BL00162	Eukaryotic-type carbonic anhydrases proteins.	BL00162C 17.78 1.000e-40 88-125 BL00162E 14.93 7.231e-39 171-204 BL00162F 22.68 5.050e-31 208-242 BL00162A 22.92 8.714e-30 16-47 BL00162D 15.06 7.158e-24 126-151 BL00162B 21.43 1.375e-19 51-74
1568	PR00457	ANIMAL HAEM PEROXIDASE SIGNATURE	PR00457E 20.67 1.621e-24 414-441 PR00457D 16.81 8.258e-21



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			389-410 PR00457B 13.29 3.455e-18 223-239 PR00457G 17.45 7.000e-18 595-616 PR00457C 19.25 4.414e-16 371-390 PR00457H 15.90 8.650e-14 666-681 PR00457A 15.80 5.645e-12 169-181 PR00457F 13.69 8.875e-11 467-478
1569	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.571e-11 50-64
1569	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 3.769e-10 50-73
1569	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE	PR00757A 6.64 5.552e-10 50-70
1569	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 2.929e-09 50-69
1569	PR00420	AROMATIC-RING HYDROXYLASE (FLAVOPROTEIN MONOOXYGENASE) SIGNATURE	PR00420A 14.78 6.455e-09 50-73
1569	BL00064	L-lactate dehydrogenase proteins.	BL00064A 21.16 7.203e-09 50-88
1569	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370A 3.35 9.772e-09 50-66
1571	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 3.880e-17 145-175
1573	BL00893	mutT domain proteins.	BL00893 18.99 5.500e-16 127-152
1573	PR00502	MUTT DOMAIN SIGNATURE	PR00502B 15.92 4.600e-13 138-154 PR00502A 15.06 2.636e-09 124-139
1574	PF00632	HECT-domain (ubiquitin-transferase).	PF00632B 18.45 7.000e-16 488-516 PF00632C 20.66 7.851e-14 533-565
1576	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 9.566e-10 292-304
1576	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 5.632e-09 243-292
1576	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.118e-11 296-329 DM00215 19.43 9.647e-11 327-360 DM00215 19.43 8.232e-10 322-355 DM00215 19.43 2.068e-09 291-324 DM00215 19.43 2.983e-09 265-298 DM00215 19.43 4.356e-09 292-325 DM00215 19.43 7.712e-09 275-308 DM00215 19.43 8.017e-09 266-299 DM00215 19.43 8.475e-09 271-304 DM00215 19.43 8.780e-09 286-319
1582	BL01280	Glucose inhibited division protein A family proteins.	BL01280A 15.97 6.727e-36 69-110 BL01280B 23.56 8.105e-27 128-180
1582	BL00076	Pyridine nucleotide-disulphide oxidoreductases class-I.	BL00076A 18.83 6.745e-12 68-98
1582	BL00836	Alanine dehydrogenase & pyridine nucleotide transhydrogenase.	BL00836D 22.30 9.576e-12 69-106
1582	BL00504	Fumarate reductase / succinate dehydrogenase FAD-binding site proteins.	BL00504A 10.76 3.870e-11 69-91
1582	BL00977	FAD-dependent glycerol-3-phosphate dehydrogenase proteins.	BL00977A 20.76 8.583e-11 69-121

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1582	PR00411	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-I SIGNATURE	PR00411A 15.95 1.000e-10 69-92
1582	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 2.151e-10 71-103
1582	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 8.846e-13 69-92 PR00368C 15.74 5.263e-10 69-95
1582	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419A 14.89 3.571e-09 69-92
1582	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE	PR00757A 6.64 6.226e-09 69-89
1582	PR00469	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-II SIGNATURE	PR00469A 15.46 1.851e-10 69-92 PR00469F 16.51 8.063e-09 65-90
1582	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 8.586e-09 69-88
1586	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 6.714e-09 70-87
1587	PD01861	PROTEIN NUCLEAR RIBONUCLEOPROTEIN SMALL MRNA RNA.	PD01861A 14.06 6.318e-10 60-84
1588	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESNA.	PD00289 9.97 6.586e-09 46-60
1588	PF00595	PDZ domain proteins (Also known as DHR or GLGF).	PF00595 13.40 9.400e-09 43-54
1591	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 1.250e-29 184-234
1592	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 6.667e-11 363-374
1592	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 6.538e-16 358-374 BL01187A 9.98 3.250e-09 278-290
1592	BL00022	EGF-like domain proteins.	BL00022B 7.54 8.200e-09 367-374
1593	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 4.600e-20 14-34 PR00625B 13.48 8.759e-20 46-67
1593	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 4.176e-18 18-35 BL00636B 15.11 1.000e-15 46-67
1594	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 3.854e-09 351-390
1598	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 1.511e-20 50-89 PD02448B 10.17 8.071e-19 89-137
1602	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 9.816e-11 144-159 PR00403B 12.19 8.167e-10 103-118
1602	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.644e-09 23-56
1602	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 5.224e-10 144-159 BL01159 13.85 6.891e-09 103-118
1602	PR00571	ENDOTHELIN-B RECEPTOR SIGNATURE	PR00571G 5.36 7.750e-09 107-126
1603	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 9.816e-11 107-122
1603	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 5.224e-10 107-122
1603	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.644e-09 23-56
1605	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929B 4.38 4.600e-10 358-370
1605	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 7.708e-10 306-

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			356 DM00303A 13.20 2.912e-09 304-354 DM00303A 13.20 7.212e-09 300-350 DM00303A 13.20 7.212e-09 311-361
1605	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354B 3.16 7.722e-09 357-370
1606	PD02379	AMINOTRANSFERASE BIOSYNTHESIS PHOSPHOSERINE SER.	PD02379E 11.43 1.000e-40 194-236 PD02379F 18.62 6.029e-35 245-284 PD02379H 16.03 5.235e-33 352-385 PD02379B 12.05 3.613e-31 80-113 PD02379A 15.57 2.800e-25 29-60 PD02379C 13.34 3.700e-21 119-139 PD02379D 11.83 9.419e-16 168-181 PD02379G 10.62 2.537e-14 313-328
1606	PR00800	AROMATIC-L-AMINO-ACID DECARBOXYLASE SIGNATURE	PR00800G 11.29 1.889e-09 97-118
1607	PD02379	AMINOTRANSFERASE BIOSYNTHESIS PHOSPHOSERINE SER.	PD02379E 11.43 1.000e-40 194-236 PD02379F 18.62 6.029e-35 245-284 PD02379B 12.05 3.613e-31 80-113 PD02379A 15.57 2.800e-25 29-60 PD02379H 16.03 7.864e-23 306-339 PD02379C 13.34 3.700e-21 119-139 PD02379D 11.83 9.419e-16 168-181
1607	PR00800	AROMATIC-L-AMINO-ACID DECARBOXYLASE SIGNATURE	PR00800G 11.29 1.889e-09 97-118
1610	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 6.625e-09 33-48
1614	BL00035	'POU' domain proteins.	BL00035B 14.46 6.236e-09 683-704
1616	PF00168	C2 domain proteins.	PF00168C 27.49 8.412e-13 634-660
1616	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.105e-10 651-665
1617	PF00168	C2 domain proteins.	PF00168C 27.49 8.412e-13 115-141
1617	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.105e-10 132-146
1619	PR00566	DOPAMINE 1B RECEPTOR SIGNATURE	PR00566E 13.44 5.255e-18 466-483 PR00566A 9.32 3.000e-17 200-214 PR00566D 9.35 1.600e-12 446-455 PR00566C 11.44 2.184e-12 401-412 PR00566B 8.20 3.053e-11 341-351
1619	PR00242	DOPAMINE RECEPTOR SIGNATURE	PR00242E 13.29 1.000e-12 424-439 PR00242B 11.77 8.650e-11 257-267
1619	BL00237	G-protein coupled receptors proteins.	BL00237C 13.19 6.786e-20 364-391 BL00237A 27.68 9.710e-15 266-306 BL00237B 5.28 5.263e-10 309-321
1619	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 5.800e-19 369-394 PR00237B 13.50 6.250e-19 236-258 PR00237E 13.03 9.500e-15 301-325 PR00237C 15.69

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			3.925e-09 280-303 PR00237A 11.48 7.387e-09 202-227
1620	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 7.851e-11 46-66
1621	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 7.529e-11 183-216
1621	PF00685	Sulfotransferase proteins.	PF00685C 26.03 5.100e-09 118-164
1621	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.322e-09 198-213
1622	BL00951	ER lumen protein retaining receptor proteins.	BL00951B 14.23 1.670e-09 43-74
1623	BL00292	Cyclins proteins.	BL00292B 20.31 3.925e-11 120-151
1624	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.160e-09 111-125
1624	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.739e-12 114-131 BL00028 16.07 3.571e-09 145-162
1625	BL01226	Hydroxymethylglutaryl-coenzyme A synthase proteins.	BL01226I 25.06 8.560e-09 256-304
1629	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.563e-12 72-91 BL00030A 14.39 2.125e-12 156-175
1637	BL00740	MAM domain proteins.	BL00740B 19.76 3.813e-09 637-658
1637	PR00597	GELSOLIN FAMILY SIGNATURE	PR00597G 8.55 6.586e-27 637-660 PR00597A 12.96 5.846e-26 326-348 PR00597E 13.46 2.000e-22 523-544 PR00597F 16.29 9.526e-22 582-602 PR00597D 12.77 1.000e-20 469-490 PR00597B 9.78 2.500e-20 415-432 PR00597C 14.19 6.192e-20 436-455 PR00597H 15.32 7.577e-19 666-686 PR00597D 12.77 3.392e-10 94-115 PR00597B 9.78 9.455e-10 36-53 PR00597C 14.19 7.875e-09 61-80 PR00597A 12.96 8.027e-09 689-711
1641	BL00027	'Homeobox' domain proteins.	BL00027 26.43 7.000e-11 93-136
1641	PR00887	STRUCTURE-SPECIFIC RECOGNITION PROTEIN SIGNATURE	PR00887D 15.12 8.909e-09 337-351
1646	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259A 9.27 3.308e-18 19-43 PR00259C 16.40 9.800e-18 88-117 PR00259D 13.50 2.756e-15 238-265
1646	BL00421	Transmembrane 4 family proteins.	BL00421A 11.79 5.263e-14 15-34 BL00421E 20.97 4.632e-13 235-265
1651	PR00669	INHIBIN ALPHA CHAIN SIGNATURE	PR00669F 5.57 9.899e-09 223-241
1652	DM01292	ESICULAR LUMEN DOMAIN.	DM01292L 12.54 9.505e-09 240-265
1653	PR00128	COLIPASE SIGNATURE	PR00128D 9.77 6.250e-25 47-66 PR00128C 9.28 5.299e-20 24-47
1653	BL00121	Colipase proteins.	BL00121B 9.96 3.160e-33 15-64 BL00121A 14.56 2.107e-09 16-56
1656	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.929e-10 384-

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			399
1658	BL01118	Translation initiation factor eIF1 proteins.	BL01118B 26.75 8.579e-26 94-132 BL01118A 12.46 4.000e-13 77-92
1659	BL00811	Oleosins proteins.	BL00811A 8.26 3.310e-09 120-158
1660	BL00674	AAA-protein family proteins.	BL00674B 4.46 9.182e-11 184-206
1660	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 8.544e-10 191-211
1660	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 9.416e-09 187-206
1660	PR00051	BACTERIAL CHROMOSOMAL REPLICATION INITIATOR (DNAA) SIGNATURE	PR00051A 10.68 9.899e-09 184-205
1661	DM01871	kw SSR LIGASE CYCLO FORMYLTETRAHYDROFOLATE.	DM01871C 20.79 9.836e-10 270-296
1663	PR00049	WILMS TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.712e-09 95-110
1665	BL01181	Ribosomal protein S21 proteins.	BL01181 15.43 2.500e-10 13-49
1666	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259C 16.40 6.824e-16 88-117 PR00259A 9.27 3.423e-14 24-48 PR00259D 13.50 1.574e-13 238-265 PR00259B 14.81 8.714e-13 61-88
1666	BL00421	Transmembrane 4 family proteins.	BL00421B 17.62 4.600e-19 67-106 BL00421E 20.97 6.211e-13 235-265 BL00421A 11.79 5.600e-12 20-39
1668	PR00496	NAPIN SIGNATURE	PR00496A 6.68 6.276e-09 21-43
1671	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 2.543e-11 670-697 PR00237A 11.48 3.000e-10 424-449
1671	PR00373	GLYCOPROTEIN HORMONE RECEPTOR SIGNATURE	PR00373D 11.16 2.403e-09 503-518
1671	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 6.600e-10 496-536 BL00237D 11.23 4.545e-09 680-697
1671	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 7.429e-09 400-413
1671	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 6.000e-11 94-108 PR00019A 11.19 7.300e-11 215-229 PR00019B 11.36 6.850e-10 46-60 PR00019A 11.19 8.043e-10 285-299 PR00019B 11.36 5.320e-09 212-226 PR00019B 11.36 9.640e-09 70-84
1672	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 7.500e-20 36-54 BL00972D 22.55 6.806e-16 296-321 BL00972B 9.45 1.000e-13 116-126 BL00972E 20.72 8.773e-12 321-343
1673	PF00646	F-box domain proteins.	PF00646A 14.37 6.906e-09 92-106
1675	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933D 24.01 7.545e-15 212-249 BL00933B 15.94 2.200e-09 54-65 BL00933E 13.80 3.543e-09 439-455 BL00933A 17.50

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			4.857e-09 20-44
1676	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 1.887e-10 137-151
1676	BL00026	Chitin recognition or binding domain proteins.	BL00026 12.95 2.776e-09 55-76
1676	BL01208	VWFC domain proteins.	BL01208B 15.83 2.946e-09 172-187
1676	BL01282	BIR repeat proteins.	BL01282B 30.49 4.471e-09 130-169
1676	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875B 5.24 4.649e-09 137-145
1676	BL00956	Fungal hydrophobins proteins.	BL00956B 8.29 4.682e-09 153-165
1676	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 6.564e-10 1-11 PD00866L 3.73 1.443e-09 33-43 PD00866L 3.73 2.918e-09 12-22 PD00866L 3.73 2.918e-09 19-29 PD00866L 3.73 4.836e-09 149-159
1676	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 6.288e-09 141-169
1676	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 7.465e-10 17-37 DM01724 8.14 4.434e-09 19-39 DM01724 8.14 6.684e-09 10-30
1676	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 5.883e-09 155-174 PR00858B 5.93 8.085e-09 136-155
1676	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 9.739e-10 125-140 PR00874C 4.37 9.000e-09 135-150
1676	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 3.779e-10 38-81 BL00243I 31.77 4.309e-10 68-111 BL00243I 31.77 5.235e-10 58-101 BL00243I 31.77 7.353e-10 98-141 BL00243I 31.77 1.000e-09 78-121 BL00243I 31.77 1.000e-09 88-131 BL00243I 31.77 1.380e-09 121-164 BL00243I 31.77 2.648e-09 119-162 BL00243I 31.77 3.662e-09 61-104 BL00243I 31.77 4.296e-09 131-174 BL00243I 31.77 4.676e-09 48-91 BL00243I 31.77 6.704e-09 109-152 BL00243I 31.77 7.845e-09 25-68 BL00243I 31.77 9.366e-09 134-177
1676	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 3.885e-16 128-174 BL00203 13.94 8.607e-13 123-169 BL00203 13.94 2.780e-11 153-199 BL00203 13.94 3.571e-11 148-194 BL00203 13.94 4.363e-11 113-159 BL00203 13.94 5.451e-11 139-185 BL00203 13.94 6.934e-11 144-190 BL00203 13.94 9.209e-11 131-177 BL00203 13.94 2.436e-10 35-81 BL00203 13.94 4.255e-10 133-179 BL00203

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			13.94 6.745e-10 32-78 BL00203 13.94 7.032e-10 154-200 BL00203 13.94 2.929e-09 34-80 BL00203 13.94 3.388e-09 149-195 BL00203 13.94 3.571e-09 136-182 BL00203 13.94 5.224e-09 127-173 BL00203 13.94 5.776e-09 43-89 BL00203 13.94 6.878e-09 140-186 BL00203 13.94 7.796e-09 45-91 BL00203 13.94 9.541e-09 42-88
1679	PD01976	KINASE DEHYDROGENASE TRANSFERASE.	PD01976A 8.95 1.493e-09 83-96
1680	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 9.859e-10 12-31
1680	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419A 14.89 4.729e-09 12-35
1680	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 9.357e-09 12-35
1683	BL01172	Ribosomal protein L44e proteins.	BL01172B 14.10 8.909e-38 15-57 BL01172C 16.78 7.188e-31 63-102
1685	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 5.909e-11 11-31 DM01724 8.14 6.591e-11 41-61 DM01724 8.14 6.831e-10 39-59 DM01724 8.14 8.697e-09 55-75
1686	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 8.463e-09 73-88
1690	PD02269	CYTIDINE DEAMINASE HYDROLASE ZINC AMINOHY.	PD02269C 16.36 7.882e-17 79-92 PD02269A 10.06 1.000e-15 29-41 PD02269D 11.98 5.000e-14 110-125
1691	BL00790	Receptor tyrosine kinase class V proteins.	BL00790D 12.41 8.297e-09 429-454
1692	BL00750	Chaperonins TCP-1 proteins.	BL00750B 16.17 2.000e-39 69-119 BL00750A 20.07 8.286e-36 25-68 BL00750C 25.65 8.579e-23 152-184
1692	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304C 8.69 1.250e-18 86-106 PR00304B 11.60 2.059e-17 56-75 PR00304A 9.20 3.605e-15 34-51
1692	PR00298	60 KD CHAPERONIN SIGNATURE	PR00298B 13.59 7.353e-11 88-116
1692	BL00296	Chaperonins cpn60 proteins.	BL00296B 15.98 4.115e-13 76-130 BL00296A 17.20 5.648e-10 12-66
1694	BL00415	Synapsins proteins.	BL00415N 4.29 4.710e-10 225-269
1694	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 5.875e-10 243-261
1694	BL00795	Involucrin proteins.	BL00795C 17.06 7.698e-10 213-258
1694	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.384e-09 247-265
1694	DM00406	GLIADIN.	DM00406 7.73 9.800e-09 245-258
1696	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-09 212-229 BL00028 16.07 6.143e-09 365-382

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1700	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.143e-13 332-351
1700	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 6.943e-09 44-485
1701	PF00023	Ank repeat proteins.	PF00023A 16.03 8.500e-10 283-299 PF00023A 16.03 9.625e-10 347-363 PF00023A 16.03 1.321e-09 184-200 PF00023A 16.03 1.643e-09 150-166
1701	BL00906	Uroporphyrinogen decarboxylase proteins.	BL00906D 24.33 7.750e-09 212-256
1701	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 8.159e-14 117-172 PF00791B 28.49 8.319e-13 217-272 PF00791B 28.49 3.179e-12 184-239 PF00791B 28.49 5.168e-12 347-402 PF00791B 28.49 5.727e-11 250-305 PF00791B 28.49 2.817e-09 17-72 PF00791B 28.49 8.514e-09 84-139 PF00791C 20.98 1.000e-08 98-137
1702	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.643e-10 202-218
1702	PF00992	Troponin.	PF00992A 16.67 9.526e-09 749-784
1708	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671C 4.18 8.966e-09 212-232
1709	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 7.805e-12 292-315
1710	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412C 11.30 2.421e-12 169-183 PR00412A 13.23 7.947e-12 104-123 PR00412B 12.59 7.429e-10 123-139
1711	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 7.247e-10 293-309
1712	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.122e-09 277-292 PR00320A 16.74 9.780e-09 233-248 PR00320C 13.01 1.000e-08 233-248
1713	BL01230	RNA methyltransferase trmA family proteins.	BL01230E 15.79 2.918e-11 487-503
1719	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 2.957e-09 434-480
1719	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 7.830e-09 408-455
1721	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 2.957e-10 33-51
1721	PR00527	GASTRIN RECEPTOR SIGNATURE	PR00527I 5.36 6.559e-09 419-439
1721	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 6.870e-09 381-400
1721	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE	PR00477I 8.53 1.000e-08 168-186
1725	PR00493	BREAST CANCER TYPE I SUSCEPTIBILITY PROTEIN SIGNATURE	PR00493G 7.57 3.711e-14 693-714
1726	BL00443	Glutamine amidotransferases class-II proteins.	BL00443F 16.68 8.714e-09 85-101
1728	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.288e-10 167-



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		PROTEIN.	187
1728	DM00215	PROLINE-RICH PROTEIN	DM00215 19.43 3.411e-10 331-364 DM00215 19.43 7.107e-10 336-369 DM00215 19.43 9.679e-10 335-368 DM00215 19.43 3.136e-09 342-375 DM00215 19.43 5.119e-09 315-348 DM00215 19.43 8.322e-09 326-359
1728	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.627e-09 335-350
1728	BL00048	Protamine P1 proteins.	BL00048 6.39 5.026e-10 152-179 BL00048 6.39 6.329e-10 173-200 BL00048 6.39 8.224e-10 161-188 BL00048 6.39 3.363e-09 155-182 BL00048 6.39 3.475e-09 163-190 BL00048 6.39 3.925e-09 167-194 BL00048 6.39 4.150e-09 151-178 BL00048 6.39 4.150e-09 159-186 BL00048 6.39 4.825e-09 171-198 BL00048 6.39 5.838e-09 176-203 BL00048 6.39 8.200e-09 177-204 BL00048 6.39 9.550e-09 153-180
1728	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 1.827e-11 345-366 PR00211B 0.86 3.571e-11 339-360 PR00211B 0.86 6.917e-09 325-346 PR00211B 0.86 1.000e-08 351-372
1731	BL01221	PMP-22 / EMP / MP20 family proteins.	BL01221C 26.20 1.281e-34 59-104 BL01221D 13.99 5.966e-27 136-163 BL01221A 17.26 2.385e-26 1-29 BL01221B 13.29 1.000e-14 38-52
1733	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.000e-10 297-340
1733	PR00024	HOMEBOX SIGNATURE	PR00024A 11.87 4.150e-09 289-301
1734	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.000e-10 297-340
1734	PR00024	HOMEBOX SIGNATURE	PR00024A 11.87 4.150e-09 289-301
1738	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 5.075e-13 73-110
1738	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.400e-12 85-98 BL00018 7.41 8.043e-09 49-62
1738	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.582e-09 44-66 PR00450C 12.22 9.772e-09 80-102
1740	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941C 19.96 4.960e-16 84-139 PD01941B 15.02 2.093e-11 4-51
1742	BL00672	Serine proteases, V8 family, histidine proteins.	BL00672B 9.84 3.554e-09 214-231
1742	PR00839	V8 SERINE PROTEASE FAMILY SIGNATURE	PR00839E 12.04 8.062e-09 213-230
1745	BL00674	AAA-protein family proteins.	BL00674B 4.46 7.814e-10 360-382
1745	DM01022	LRR REPEAT.	DM01022A 7.35 1.900e-09 954-

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			961
1745	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.186e-09 267-282
1746	BL00674	AAA-protein family proteins.	BL00674B 4.46 7.814e-10 360-382
1746	DM01022	LRR REPEAT.	DM01022A 7.35 1.900e-09 954-961
1746	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.186e-09 267-282
1747	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.591e-18 206-231 BL00215A 15.82 4.000e-15 104-129 BL00215A 15.82 9.400e-15 7-32 BL00215B 10.44 1.000e-10 154-167
1747	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927G 11.07 9.036e-11 158-174 PR00927B 14.66 4.652e-10 239-261
1747	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 2.826e-09 9-32 PR00926F 17.75 3.217e-09 208-231
1749	BL01013	Oxysterol-binding protein family proteins.	BL01013A 25.14 5.500e-21 537-573 BL01013D 26.81 2.161e-18 807-851 BL01013C 9.97 4.231e-13 625-635 BL01013B 11.33 3.017e-11 603-614
1751	BL00711	Lipoxygenases iron-binding region proteins.	BL00711I 18.56 8.630e-28 577-615 BL00711E 19.66 3.550e-22 414-451 BL00711G 21.83 9.100e-22 503-535 BL00711C 20.75 5.959e-19 268-297 BL00711D 17.56 1.923e-16 347-373 BL00711H 23.34 1.771e-12 535-574 BL00711F 19.79 2.086e-10 484-501
1751	PR00087	LIPOXYGENASE SIGNATURE	PR00087C 15.00 1.184e-17 423-444 PR00087A 18.37 7.061e-12 385-403 PR00087B 15.25 5.091e-10 403-421
1751	PR00467	MAMMALIAN LIPOXYGENASE SIGNATURE	PR00467E 9.00 3.400e-14 344-364 PR00467D 16.69 4.082e-09 243-265
1753	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE	PR00492C 9.68 1.900e-23 122-139 PR00492B 9.77 8.579e-23 76-95 PR00492D 14.82 8.200e-21 139-155 PR00492A 11.92 1.643e-18 60-76
1756	BL00378	Hexokinases proteins.	BL00378A 19.01 8.500e-09 403-431
1757	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.615e-33 35-78
1757	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 4.259e-27 24-63 BL00032C 11.28 5.909e-20 63-81
1757	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 4.000e-11 21-37
1757	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.960e-11 58-75
1757	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 9.357e-13 67-77 PR00024B 11.27 3.500e-11 57-68 PR00024A 11.87 9.400e-11 42-54

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1758	PR00179	LIPOCALIN SIGNATURE	PR00179B 9.56 1.000e-12 102-115 PR00179C 19.02 1.000e-10 130-146 PR00179A 13.78 5.680e-10 37-50
1758	BL00213	Lipocalin proteins.	BL00213B 8.78 8.000e-10 102-113 BL00213A 12.95 9.526e-10 37-51
1759	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 1.818e-11 164-187
1762	BL00269	Mammalian defensins proteins.	BL00269C 16.52 7.158e-09 171-200
1762	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 5.855e-10 57-85 PD02283C 17.54 5.855e-10 87-115 PD02283C 17.54 6.566e-10 117-145 PD02283C 17.54 1.450e-09 47-75 PD02283C 17.54 1.450e-09 77-105 PD02283C 17.54 1.450e-09 107-135 PD02283C 17.54 5.613e-09 67-95 PD02283C 17.54 5.613e-09 97-125 PD02283C 17.54 6.175e-09 137-165 PD02283C 17.54 7.525e-09 37-65 PD02283C 17.54 8.875e-09 147-175
1762	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 3.379e-12 95-141 BL00203 13.94 3.690e-12 65-111 BL00203 13.94 2.978e-11 35-81 BL00203 13.94 5.549e-11 39-85 BL00203 13.94 6.538e-11 55-101 BL00203 13.94 6.538e-11 85-131 BL00203 13.94 7.231e-11 34-80 BL00203 13.94 7.429e-11 125-171 BL00203 13.94 7.527e-11 69-115 BL00203 13.94 8.220e-11 99-145 BL00203 13.94 1.670e-10 64-110 BL00203 13.94 2.053e-10 94-140 BL00203 13.94 2.149e-10 124-170 BL00203 13.94 2.819e-10 159-205 BL00203 13.94 5.213e-10 54-100 BL00203 13.94 5.213e-10 84-130 BL00203 13.94 5.691e-10 59-105 BL00203 13.94 5.691e-10 89-135 BL00203 13.94 6.936e-10 129-175 BL00203 13.94 7.511e-10 115-161 BL00203 13.94 7.702e-10 49-95 BL00203 13.94 7.702e-10 79-125 BL00203 13.94 1.551e-09 44-90 BL00203 13.94 1.551e-09 74-120 BL00203 13.94 3.112e-09 29-75 BL00203 13.94 4.031e-09 30-76 BL00203 13.94 4.214e-09 90-136 BL00203 13.94 4.306e-09 60-106 BL00203 13.94 5.133e-09 145-191 BL00203 13.94 6.235e-09 119-165 BL00203 13.94 6.327e-09 50-96 BL00203 13.94 6.327e-09 80-126 BL00203 13.94

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			6.694e-09 43-91 BL00203 13.94 6.694e-09 75-121 BL00203 13.94 8.898e-09 101-150
1763	BL00216	Sugar transport proteins.	BL00216B 21.64 5.846e-09 141-191
1766	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 2.080e-30 83-138 BL00456C 24.55 3.721e-29 221-276 BL00456B 18.94 1.000e-22 159-189
1766	PR00175	SODIUM/ALANINE SYMPORTER SIGNATURE	PR00175B 10.80 9.878e-09 226-245
1767	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 1.857e-09 494-505
1768	BL00509	Ras GTPase-activating proteins.	BL00509B 10.28 1.643e-12 610-621
1772	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.143e-13 252-266 PR00048A 10.52 7.429e-13 476-490 PR00048A 10.52 3.118e-12 336-350 PR00048A 10.52 3.118e-12 364-378 PR00048A 10.52 4.706e-12 504-518 PR00048A 10.52 8.412e-12 224-238 PR00048A 10.52 3.842e-11 392-406 PR00048A 10.52 6.211e-11 308-322 PR00048A 10.52 6.211e-11 448-462 PR00048B 6.02 7.231e-11 492-502 PR00048B 6.02 3.250e-10 240-250 PR00048A 10.52 6.870e-10 420-434 PR00048B 6.02 2.421e-09 380-390
1772	PD00066	PROTEIN ZINC-FINGER METAL-BINDI	PD00066 13.92 8.800e-14 327-340 PD00066 13.92 1.500e-13 411-424 PD00066 13.92 5.500e-13 383-396 PD00066 13.92 5.500e-13 439-452 PD00066 13.92 7.500e-13 495-508 PD00066 13.92 9.000e-13 467-480 PD00066 13.92 3.571e-12 355-368 PD00066 13.92 7.000e-12 271-284 PD00066 13.92 7.923e-10 299-312 PD00066 13.92 2.500e-09 243-256
1772	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.250e-13 395-412 BL00028 16.07 5.950e-13 367-384 BL00028 16.07 6.478e-12 451-468 BL00028 16.07 8.435e-12 339-356 BL00028 16.07 1.692e-11 255-272 BL00028 16.07 3.769e-11 227-244 BL00028 16.07 5.154e-11 507-524 BL00028 16.07 2.200e-10 479-496 BL00028 16.07 9.400e-10 199-216 BL00028 16.07 2.029e-09 423-440 BL00028 16.07 3.571e-09 311-328
1773	PR00122	VACUOLAR ATP SYNTHASE 16 KD	PR00122D 9.97 7.214e-11 103-

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		SUBUNIT SIGNATURE	127 PR00122C 8.20 9.526e-10 76-103
1773	BL00605	ATP synthase c subunit proteins.	BL00605 27.67 4.977e-09 70-124
1774	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39
1776	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.610e-09 33-87 BL01160B 19.54 9.619e-09 65-119
1783	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 6.786e-15 3967-4001
1783	PF00856	SET domain proteins.	PF00856B 16.42 6.595e-19 3949-3971 PF00856A 26.14 4.125e-12 3896-3933
1783	PF00628	PHD-finger.	PF00628 15.84 3.455e-12 86-101 PF00628 15.84 7.750e-10 38-53 PF00628 15.84 5.645e-09 164-179
1783	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 4.971e-09 2575-2624 BL00115Z 3.12 7.750e-09 2582-2631
1784	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 9.423e-10 111-124
1785	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e-10 177-191
1790	PF00922	Vesiculovirus phosphoprotein.	PF00922A 19.17 7.724e-09 276-310
1792	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059A 28.10 5.950e-10 34-75
1794	BL00326	Tropomyosins proteins.	BL00326D 8.76 8.065e-09 165-206
1795	BL00326	Tropomyosins proteins.	BL00326D 8.76 8.065e-09 173-214
1797	PR00563	BETA-3 ADRENERGIC RECEPTOR SIGNATURE	PR00563B 3.98 8.141e-09 8-28
1799	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.570e-09 285-307
1801	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.800e-14 290-303 PD00066 13.92 4.000e-13 234-247 PD00066 13.92 4.429e-12 262-275 PD00066 13.92 9.217e-11 206-219 PD00066 13.92 3.769e-10 505-518 PD00066 13.92 4.115e-10 449-462 PD00066 13.92 4.462e-10 533-546 PD00066 13.92 6.538e-10 477-490
1801	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.091e-15 243-257 PR00048A 10.52 7.750e-14 542-556 PR00048A 10.52 3.647e-12 215-229 PR00048A 10.52 4.176e-12 486-500 PR00048B 6.02 6.000e-12 231-241 PR00048B 6.02 6.000e-12 287-297 PR00048A 10.52 7.353e-12 187-201 PR00048A 10.52 6.684e-11 271-285 PR00048A 10.52 4.130e-10 299-313 PR00048A 10.52 3.520e-09 430-444 PR00048A 10.52 3.880e-09 514-

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			528 PR00048A 10.52 6.400e-09 458-472 PR00048A 10.52 8.560e-09 159-173
1801	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.563e-15 545-562 BL00028 16.07 1.450e-13 218-235 BL00028 16.07 3.348e-12 489-506 BL00028 16.07 7.652e-12 274-291 BL00028 16.07 2.385e-11 433-450 BL00028 16.07 4.115e-11 517-534 BL00028 16.07 5.154e-11 246-263 BL00028 16.07 1.000e-10 302-319 BL00028 16.07 5.200e-10 461-478 BL00028 16.07 6.700e-10 190-207 BL00028 16.07 1.257e-09 357-374 BL00028 16.07 9.486e-09 162-179
1802	BL00615	C-type lectin domain proteins.	BL00615A 16.68 8.920e-11 137-155
1802	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE	PR00770F 13.79 1.774e-09 198-218
1802	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 2.521e-09 137-155
1803	BL00615	C-type lectin domain proteins.	BL00615A 16.68 8.920e-11 176-194
1803	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE	PR00770F 13.79 1.774e-09 237-257
1803	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 2.521e-09 176-194
1804	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 9.000e-14 65-78
1806	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.000e-09 219-233
1808	PD02474	SYNTHASE SMALL SUBUNIT ACETOLACT.	PD02474B 21.08 8.568e-09 199-238
1809	PF00922	Vesiculovirus phosphoprotein.	PF00922A 19.17 1.000e-08 249-283
1812	PR00289	DISINTEGRIN SIGNATURE	PR00289B 11.79 1.947e-09 522-535
1814	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242F 12.18 8.522e-09 197-219
1815	PR00780	LEUSERPIN 2 SIGNATURE	PR00780B 4.89 4.491e-09 262-285
1816	BL00226	Intermediate filaments proteins.	BL00226D 19.10 8.027e-13 208-255
1817	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 3.326e-15 481-534 PD01876C 21.73 3.045e-10 735-788
1818	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747C 12.06 8.767e-09 337-356
1820	DM01782	HYDROGENASE (FE) LARGE CHAIN.	DM01782C 13.88 4.400e-19 349-368 DM01782F 9.01 4.375e-18 499-515 DM01782B 17.29 3.412e-10 294-327
1821	BL00226	Intermediate filaments proteins.	BL00226D 19.10 7.375e-38 321-368 BL00226B 23.86 7.107e-32 155-203 BL00226C 13.23 3.100e-

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			19 220-251 BL00226A 12.77 7.000e-15 55-70 BL00226D 19.10 7.800e-09 254-301
1822	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415B 13.78 9.518e-10 4-52
1822	BL00026	Chitin recognition or binding domain proteins.	BL00026 12.95 3.013e-09 43-64
1822	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 3.588e-09 110-138 PD02283C 17.54 3.588e-09 120-148
1822	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 1.443e-09 21-31 PD00866L 3.73 2.770e-09 97-107 PD00866L 3.73 2.770e-09 146-156 PD00866L 3.73 2.918e-09 7-17 PD00866L 3.73 2.918e-09 14-24 PD00866L 3.73 4.541e-09 4-14
1822	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 2.819e-09 84-103 PR00858B 5.93 5.021e-09 114-133 PR00858B 5.93 5.021e-09 124-143
1822	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875B 5.24 6.595e-09 85-93
1822	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 9.739e-10 73-88 PR00874C 4.37 7.250e-09 83-98
1822	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 3.143e-11 13-56 BL00243I 31.77 3.647e-10 26-69 BL00243I 31.77 6.426e-10 106-149 BL00243I 31.77 7.088e-10 96-139 BL00243I 31.77 9.338e-10 36-79 BL00243I 31.77 1.254e-09 46-89 BL00243I 31.77 6.451e-09 3-46 BL00243I 31.77 6.704e-09 77-120 BL00243I 31.77 7.211e-09 67-110 BL00243I 31.77 7.592e-09 116-159 BL00243I 31.77 8.606e-09 92-135
1822	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 9.700e-09 6-18
1822	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 8.024e-14 102-148 BL00203 13.94 7.750e-13 127-173 BL00203 13.94 1.103e-12 97-143 BL00203 13.94 3.172e-12 103-149 BL00203 13.94 3.379e-12 92-138 BL00203 13.94 4.207e-12 98-144 BL00203 13.94 4.207e-12 116-162 BL00203 13.94 5.345e-12 71-117 BL00203 13.94 5.345e-12 107-153 BL00203 13.94 9.897e-12 106-152 BL00203 13.94 1.791e-11 118-164 BL00203 13.94 2.879e-11 126-172 BL00203 13.94 3.176e-11 87-133 BL00203 13.94 4.758e-11 61-107 BL00203 13.94 5.846e-11 113-159 BL00203 13.94 6.044e-11 112-158 BL00203 13.94 7.231e-11 93-139 BL00203 13.94 1.287e-10

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			128-174 BL00203 13.94 2.245e-10 76-122 BL00203 13.94 3.202e-10 23-69 BL00203 13.94 4.926e-10 78-124 BL00203 13.94 6.362e-10 81-127 BL00203 13.94 6.553e-10 82-128 BL00203 13.94 6.840e-10 111-157 BL00203 13.94 8.851e-10 43-89 BL00203 13.94 8.851e-10 96-142 BL00203 13.94 2.837e-09 8-54 BL00203 13.94 3.296e-09 72-118 BL00203 13.94 3.847e-09 117-163 BL00203 13.94 3.939e-09 86-132 BL00203 13.94 5.592e-09 123-169 BL00203 13.94 5.776e-09 108-154 BL00203 13.94 6.143e-09 30-76 BL00203 13.94 6.143e-09 79-125 BL00203 13.94 6.969e-09 121-167 BL00203 13.94 7.612e-09 16-62 BL00203 13.94 7.796e-09 101-147 BL00203 13.94 8.163e-09 33-79 BL00203 13.94 9.633e-09 77-123 BL00203 13.94 1.000e-08 66-112
1824	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860B 7.04 2.929e-20 74-88 PR00860A 5.46 5.655e-13 52-65 PR00860C 9.61 2.400e-12 88-98
1824	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 1.419e-11 70-89 PR00858B 5.93 7.070e-11 65-84
1824	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 3.478e-10 64-79
1824	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 7.875e-10 59-85 BL00243I 31.77 4.803e-09 65-108
1824	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876D 5.77 2.191e-10 62-75 PR00876A 6.60 5.886e-09 61-74
1824	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 1.000e-40 62-108 BL00203 13.94 7.429e-09 54-100 BL00203 13.94 8.071e-09 52-98 BL00203 13.94 8.806e-09 55-101
1824	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875D 5.00 9.471e-09 59-70
1825	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.136e-09 572-586
1825	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399A 9.52 8.875e-09 360-376
1829	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e-10 567-587 DM01206B 10.69 1.000e-09 563-583
1829	PD01351	PROTEIN REPEAT NEUROFILAMENT TRIPL.	PD01351B 13.72 6.786e-10 196-222 PD01351B 13.72 2.597e-09 198-224
1829	BL00035	'POU' domain proteins.	BL00035B 14.46 3.127e-09 634-655
1829	BL00229	Tau and MAP proteins tubulin-binding domain proteins.	BL00229A 23.57 3.182e-09 178-217
1829	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.647e-11 204-219 PR00049D 0.00 9.471e-11 209-224 PR00049D 0.00 8.500e-



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			10 206-221 PR00049D 0.00 8.500e-10 207-222 PR00049D 0.00 3.746e-09 182-197
1829	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 3.132e-09 265-299 BL00319C 17.12 4.553e-09 1013-1047 BL00319C 17.12 5.618e-09 1019-1053 BL00319C 17.12 7.395e-09 267-301 BL00319C 17.12 7.632e-09 1017-1051
1829	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.089e-10 185-218 DM00215 19.43 8.393e-10 190-223 DM00215 19.43 2.373e-09 186-219 DM00215 19.43 7.102e-09 183-216 DM00215 19.43 8.169e-09 188-221
1829	BL00422	Granins proteins.	BL00422C 16.18 8.588e-09 263-291
1829	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 9.182e-11 1005-1056 BL00412D 16.54 9.120e-10 1004-1055 BL00412D 16.54 4.857e-09 1003-1054 BL00412D 16.54 8.347e-09 1008-1059 BL00412D 16.54 9.449e-09 1001-1052
1829	PR00832	PAXILLIN SIGNATURE	PR00832B 9.87 9.526e-09 377-401
1829	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 9.620e-09 196-231
1829	PF00992	Troponin.	PF00992A 16.67 9.882e-09 1005-1040
1829	BL00048	Protamine P1 proteins.	BL00048 6.39 6.949e-15 569-596 BL00048 6.39 1.885e-14 568-595 BL00048 6.39 3.361e-14 570-597 BL00048 6.39 8.377e-14 577-604 BL00048 6.39 8.377e-14 578-605 BL00048 6.39 3.631e-13 571-598 BL00048 6.39 4.738e-13 576-603 BL00048 6.39 7.369e-13 582-609 BL00048 6.39 2.456e-12 575-602 BL00048 6.39 3.118e-12 573-600 BL00048 6.39 3.515e-12 567-594 BL00048 6.39 5.235e-12 581-608 BL00048 6.39 5.632e-12 583-610 BL00048 6.39 7.221e-12 557-584 BL00048 6.39 2.250e-11 572-599 BL00048 6.39 2.875e-11 585-612 BL00048 6.39 4.875e-11 586-613 BL00048 6.39 5.375e-11 591-618 BL00048 6.39 7.375e-11 589-616 BL00048 6.39 7.500e-11 580-607 BL00048 6.39 8.625e-11 588-615 BL00048 6.39 2.895e-10 563-590 BL00048 6.39 5.382e-10 574-601 BL00048 6.39 5.500e-10 566-593 BL00048 6.39 5.618e-10 584-611 BL00048 6.39 9.171e-10 561-588 BL00048 6.39 9.882e-10 592-619

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			BL00048 6.39 1.450e-09 590-617 BL00048 6.39 3.925e-09 560-587 BL00048 6.39 4.488e-09 562-589 BL00048 6.39 4.938e-09 579-606 BL00048 6.39 5.275e-09 564-591 BL00048 6.39 5.725e-09 558-585 BL00048 6.39 5.725e-09 587-614 BL00048 6.39 6.625e-09 555-582 BL00048 6.39 7.075e-09 556-583 BL00048 6.39 9.438e-09 559-586 BL00048 6.39 9.888e-09 600-627
1829	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 1.000e-08 201-219
1830	BL00092	N-6 Adenine-specific DNA methylases proteins.	BL00092 5.35 2.000e-09 136-145
1831	PR00511	TEKTIN SIGNATURE	PR00511A 13.59 3.700e-14 113-130
1833	PR00764	COMPLEMENT C9 SIGNATURE	PR00764F 16.89 2.286e-09 158-179
1833	BL00022	EGF-like domain proteins.	BL00022B 7.54 4.600e-09 138-145
1833	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 4.086e-10 167-183 BL01187B 12.04 4.600e-09 104-120
1833	BL01185	C-terminal cystine knot proteins.	BL01185B 21.14 6.929e-09 146-195
1833	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 7.429e-09 109-120 PR00010C 11.16 7.643e-09 172-183 PR00010A 11.79 8.846e-09 190-202
1833	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011A 14.06 4.822e-09 208-227 PR00011D 14.03 8.957e-09 67-86
1833	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 1.000e-08 34-77
1835	BL01279	Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa.	BL01279A 24.27 3.691e-09 419-467
1835	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 4.600e-09 421-467
1835	BL01230	RNA methyltransferase trmA family proteins.	BL01230E 15.79 6.607e-11 571-587 BL01230A 17.88 8.962e-10 409-428 BL01230B 11.62 8.475e-09 436-449
1835	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.780e-09 598-613
1837	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 2.603e-11 259-287 PD01719A 12.89 8.105e-10 199-227
1838	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.269e-18 151-195 BL01162A 15.38 1.265e-11 64-87
1838	BL00279	Membrane attack complex components / perforin proteins.	BL00279C 31.64 3.156e-09 134-188
1838	BL00059	Zinc-containing alcohol dehydrogenases proteins.	BL00059B 16.08 7.273e-09 93-121
1841	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.415e-26 46-85

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1841	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.737e-11 140-154 PR00048A 10.52 6.087e-10 224-238
1841	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.130e-12 227-244 BL00028 16.07 7.577e-11 352-369 BL00028 16.07 3.400e-10 380-397 BL00028 16.07 6.400e-10 199-216 BL00028 16.07 1.257e-09 143-160 BL00028 16.07 2.029e-09 171-188 BL00028 16.07 5.886e-09 408-425
1841	PR00967	ACUTE MYELOID LEUKEMIA 1 PROTEIN SIGNATURE	PR00967I 12.41 8.130e-09 466-481
1841	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.038e-10 187-200 PD00066 13.92 1.600e-09 396-409 PD00066 13.92 9.400e-09 215-228
1841	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 6.553e-09 214-237 BL00479A 19.86 9.809e-09 367-390
1842	PD02910	TRANSCRIPTION PROTEIN FACTOR REGULATION A.	PD02910A 15.43 9.839e-09 62-97
1843	PD02199	SUBUNIT HYDROGEN ION TRANSPORT T.	PD02199A 20.58 1.000e-40 10-61 PD02199D 13.18 1.000e-40 364-405 PD02199F 15.02 1.000e-40 440-482 PD02199J 11.42 1.000e-40 723-762 PD02199K 15.22 1.000e-40 792-831 PD02199G 9.43 4.447e-24 531-555 PD02199B 27.90 1.474e-22 263-306 PD02199H 13.62 2.636e-21 576-599 PD02199E 7.56 8.642e-19 405-424 PD02199C 17.60 8.085e-14 313-329 PD02199I 8.90 4.780e-09 616-624
1844	BL00218	Amino acid permeases proteins.	BL00218E 23.30 5.920e-10 343-383
1845	BL00048	Protamine P1 proteins.	BL00048 6.39 9.526e-10 160-187
1845	BL00422	Granins proteins.	BL00422C 16.18 4.000e-09 590-618
1845	PR00833	POLLEN ALLERGEN POA P1 SIGNATURE	PR00833H 2.30 8.385e-09 943-958
1845	PF00992	Troponin.	PF00992A 16.67 7.900e-13 568-603 PF00992A 16.67 4.090e-11 566-601 PF00992A 16.67 5.817e-10 570-605 PF00992A 16.67 8.479e-10 579-614 PF00992A 16.67 2.066e-09 564-599 PF00992A 16.67 4.789e-09 575-610 PF00992A 16.67 4.908e-09 532-567 PF00992A 16.67 6.803e-09 536-571 PF00992A 16.67 7.632e-09 562-597 PF00992A 16.67 8.697e-09 585-620 PF00992A 16.67 9.053e-09 583-618 PF00992A 16.67 9.289e-09 516-551

SEQ ID NO:	Database entry ID	Description	Results*
1845	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.500e-12 505-540 PF01140D 15.54 7.120e-11 584-619 PF01140D 15.54 9.760e-11 586-621 PF01140D 15.54 3.813e-10 588-623 PF01140D 15.54 4.938e-10 563-598 PF01140D 15.54 6.738e-10 519-554 PF01140D 15.54 8.313e-10 503-538 PF01140D 15.54 9.325e-10 549-584 PF01140D 15.54 9.663e-10 567-602 PF01140D 15.54 9.775e-10 565-600 PF01140D 15.54 1.000e-09 582-617 PF01140D 15.54 2.884e-09 575-610 PF01140D 15.54 3.198e-09 551-586 PF01140D 15.54 3.302e-09 517-552 PF01140D 15.54 4.140e-09 533-568 PF01140D 15.54 4.872e-09 578-613 PF01140D 15.54 6.860e-09 581-616 PF01140D 15.54 7.174e-09 594-629 PF01140D 15.54 7.384e-09 576-611 PF01140D 15.54 7.593e-09 572-607 PF01140D 15.54 8.640e-09 570-605 PF01140D 15.54 8.744e-09 507-542 PF01140D 15.54 8.744e-09 596-631 PF01140D 15.54 9.163e-09 577-612 PF01140D 15.54 9.267e-09 579-614 PF01140D 15.54 9.791e-09 574-609 PF01140D 15.54 1.000e-08 531-566
1848	BL00811	Oleosins proteins.	BL00811B 10.57 9.791e-09 307-336
1852	BL00415	Synapsins proteins.	BL00415N 4.29 4.153e-09 301-345
1852	DM00668	ZEIN.	DM00668B 22.01 8.018e-09 291-343
1853	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-17 133-164
1853	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109E 14.41 3.045e-11 254-277
1853	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.317e-16 689-744 PF00791B 28.49 3.753e-15 523-578 PF00791B 28.49 4.316e-12 656-711 PF00791B 28.49 1.727e-11 589-644 PF00791B 28.49 3.636e-11 556-611 PF00791C 20.98 4.913e-11 570-609 PF00791B 28.49 6.330e-10 722-777 PF00791C 20.98 5.853e-09 703-742
1853	PF00023	Ank repeat proteins.	PF00023A 16.03 5.200e-13 722-738 PF00023B 14.20 1.000e-12 652-662 PF00023A 16.03 2.000e-12 755-771 PF00023A 16.03 7.857e-11 656-672 PF00023A

SEQ ID NO:	Database entry ID	Description	Results*
			16.03 8.286e-11 622-638 PF00023B 14.20 4.682e-09 519-529 PF00023A 16.03 6.143e-09 589-605 PF00023A 16.03 6.786e-09 689-705
1853	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 9.000e-11 582-595 PD00078B 13.14 8.435e-09 649-662
1854	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 4.971e-14 4-26
1856	BL00317	WAP-type 'four-disulfide core' domain proteins.	BL00317B 14.58 3.550e-13 48-70
1856	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003C 7.69 6.357e-09 54-64
1857	BL01019	ADP-ribosylation factors family proteins.	BL01019B 19.49 7.517e-21 95-150
1857	BL01020	SAR1 family proteins.	BL01020C 15.35 2.301e-18 79-130
1857	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE	PR00328C 13.16 2.841e-10 78-104
1858	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.385e-15 128-141 PD00066 13.92 5.714e-12 100-113
1858	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 7.188e-10 97-107 PR00048B 6.02 3.842e-09 125-135 PR00048A 10.52 6.040e-09 137-151
1859	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-11 174-188 PR00048B 6.02 1.692e-11 162-172
1859	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.739e-11 165-178
1859	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.385e-11 177-194 BL00028 16.07 3.769e-11 121-138 BL00028 16.07 8.269e-11 149-166
1860	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 2.895e-11 45-58
1860	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.038e-10 419-432 PD00066 13.92 7.231e-10 391-404
1860	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.696e-10 400-414 PR00048A 10.52 8.435e-10 428-442
1860	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.269e-11 403-420 BL00028 16.07 3.400e-10 375-392 BL00028 16.07 3.057e-09 431-448
1861	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 7.643e-34 606-653 DM00547B 11.28 7.907e-16 155-169 DM00547C 17.30 8.650e-14 209-231 DM00547D 11.60 6.500e-13 277-291 DM00547E 13.94 1.000e-11 307-330
1861	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 6.379e-10 590-636
1862	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.330e-11 18-62

SEQ ID NO:	Database entry ID	Description	Results*
1862	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 1.809e-09 52-92
1862	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 3.647e-19 59-82 PR00449A 13.20 7.000e-15 38-40 PR00449D 10.79 8.875e-14 121-135 PR00449E 13.50 8.920e-14 157-180 PR00449B 14.34 8.500e-09 41-58
1867	BL01283	T-box domain proteins.	BL01283D 11.70 7.868e-31 59-92 BL01283C 13.05 2.537e-14 25-39
1867	PR00937	T-BOX DOMAIN SIGNATURE	PR00937D 13.41 5.378e-15 24-39 PR00937F 12.53 1.450e-12 83-92 PR00937E 11.86 5.592e-12 62-76 PR00937C 10.51 5.219e-10 5-15
1870	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 8.699e-09 100-121
1872	BL00470	Isocitrate and isopropylmalate dehydrogenases proteins.	BL00470A 16.25 5.179e-14 10-31 BL00470C 15.43 4.103e-10 223-238 BL00470E 16.52 1.900e-09 287-297
1873	PF00023	Ank repeat proteins.	PF00023A 16.03 3.893e-09 44-60 PF00023B 14.20 9.182e-09 40-50
1874	PF00023	Ank repeat proteins.	PF00023A 16.03 3.893e-09 72-88 PF00023B 14.20 9.182e-09 68-78
1877	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.019e-26 51-90
1877	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.786e-16 427-444 BL00028 16.07 1.900e-13 287-304 BL00028 16.07 3.700e-13 481-498 BL00028 16.07 1.000e-12 315-332 BL00028 16.07 1.000e-12 399-416 BL00028 16.07 3.348e-12 453-470 BL00028 16.07 4.522e-12 371-388 BL00028 16.07 6.885e-11 343-360 BL00028 16.07 4.600e-10 509-526
1877	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.500e-17 424-438 PR00048A 10.52 7.000e-14 312-326 PR00048A 10.52 1.643e-13 396-410 PR00048A 10.52 3.571e-13 478-492 PR00048B 6.02 9.000e-12 300-310 PR00048A 10.52 1.000e-11 506-520 PR00048A 10.52 5.737e-11 340-354 PR00048A 10.52 1.391e-10 284-298 PR00048B 6.02 6.063e-10 412-422 PR00048B 6.02 1.474e-09 494-504 PR00048B 6.02 2.895e-09 356-366
1877	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.600e-14 415-428 PD00066 13.92 7.000e-14 469-482 PD00066 13.92 5.500e-13 303-316 PD00066 13.92 4.429e-12 331-344 PD00066 13.92 9.217e-11 497-510 PD00066 13.92 2.038e-10 387-400 PD00066 13.92 6.400e-09

SEQ ID NO:	Database entry ID	Description	Results*
			359-372
1878	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 4.927e-13 222-242
1878	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 1.545e-11 218-237
1878	PR00051	BACTERIAL CHROMOSOMAL REPLICATION INITIATOR (DNAA) SIGNATURE	PR00051A 10.68 3.647e-10 215-236
1878	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 9.213e-10 217-233
1878	BL00674	AAA-protein family proteins.	BL00674B 4.46 9.000e-24 215-237 BL00674C 22.60 8.448e-20 248-291 BL00674D 23.41 5.140e-18 308-355 BL00674E 15.24 9.217e-16 390-410 BL00674A 16.91 5.304e-09 181-202
1878	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.615e-09 219-236
1879	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 1.957e-32 35-90 BL00456B 18.94 9.780e-17 111-141
1880	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 1.957e-32 35-90 BL00456C 24.55 1.225e-31 173-228 BL00456B 18.94 9.780e-17 111-141
1884	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 1.818e-11 159-182
1885	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 5.897e-10 352-372
1885	BL00847	MCM family proteins.	BL00847D 15.16 8.568e-25 343-384 BL00847B 24.76 8.971e-25 194-237 BL00847C 18.79 9.270e-10 301-335
1885	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.931e-09 346-368
1885	BL00674	AAA-protein family proteins.	BL00674B 4.46 5.378e-09 345-367
1886	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 7.000e-10 50-63
1886	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 5.295e-09 507-521
1886	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 6.625e-09 479-489
1887	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.625e-13 544-558
1887	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364B 13.94 5.500e-09 544-560
1888	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.625e-13 544-558
1888	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364B 13.94 5.500e-09 544-560
1889	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.625e-13 544-558
1889	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364B 13.94 5.500e-09 544-560
1890	PF00938	Lipoprotein.	PF00938E 19.50 6.096e-09 272-

SEQ ID NO:	Database entry ID	Description	Results*
			307
1891	PF00925	GTP cyclohydrolase II.	PF00925F 13.23 9.850e-09 356-367
1893	BL00226	Intermediate filaments proteins.	BL00226A 12.77 5.355e-13 139-154
1895	PF00035	Double-stranded RNA binding motif.	PF00035B 12.08 7.750e-09 273-287
1896	PF00622	Domain in SP1a and the RYanodine Receptor.	PF00622B 21.00 9.250e-11 170-192

**TABLE 4**

SEQ ID	Model	Description	E-value	Score	Repeats	Position
950	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	6.6e-26	99.5	1	825-886
950	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	2.5e-15	64.4	1	266-297
952	efhand	EF hand	0.0034	24.0	1	322-350
952	Adeno_E 1A	Early E1A protein	8.9	-168.3	1	298-448
953	SH2	SH2 domain	1.5e-16	68.4	1	320-396
954	SH2	SH2 domain	1.5e-16	68.4	1	347-423
955	RCC1	Regulator of chromosome condensation (RCC1)	1.3e-13	58.6	4	148-197:200-249:318-367:370-418
958	BRCT	BRCA1 C Terminus (BRCT) domain	7.2	1.2	1	45-130
962	UQ_con	Ubiquitin-conjugating enzyme	5.4e-39	143.0	1	2-117
963	UQ_con	Ubiquitin-conjugating enzyme	1.6e-57	204.5	1	2-132
971	kinesin	Kinesin motor domain	2.2e-154	526.3	1	47-372
971	WD40	WD domain, G-beta repeat	1e-53	191.9	7	1327-1361:1367-1402:1432-1466:1472-1511:1523-1557:1564-1600:1606-1640
971	filament	Intermediate filament protein	2.6	-195.6	1	423-805
971	HDV_ag	Hepatitis delta virus delta antigen	6.2	-47.5	1	703-880
971	PFEMP	Plasmodium falciparum erythrocyte membrane p	8.9	-86.8	1	475-585
971	G6PD	Glucose-6-phosphate dehydrogenase, NAD bindi	9.6	-123.8	1	912-1049
971	DUF232	Putative transcriptional regulator	9.7	-30.1	1	616-750
975	Kelch	Kelch motif	5.7e-62	219.3	4	267-312:314-359:361-406:408-453
975	BTB	BTB/POZ domain	3.1e-38	140.4	1	23-130
977	kinesin	Kinesin motor domain	9.7e-	520.8	1	53-353



SEQ ID	Model	Description	E-value	Score	Repeats	Position
			153			
977	FHA	FHA domain	0.078	16.9	1	470-534
977	KMP11	Kinetoplastid membrane protein 11	3.6	-3.2	1	355-438
977	SART-1	SART-1 family	7.1	-360.1	1	325-881
977	Transposase 22	L1 transposable element	8.1	-180.7	1	322-622
979	Ribosomal L10	Ribosomal protein L10	6	-33.3	1	70-173
980	Aa trans	Transmembrane amino acid transporter	1.6e-75	264.3	1	69-479
980	oxidored_q1	NADH-Ubiquinone/plastoquinone	7.6	-169.3	1	63-326
980	xan_ur_permease	Permease family	8.4	-201.3	1	137-471
980	Trp_Tyr_perm	Tryptophan/tyrosine permease family	9.6	-297.9	1	70-474
982	HYR	HYR domain	2e-35	131.1	2	106-187:188-267
982	EGF	EGF-like domain	3.9e-24	93.6	3	742-773:780-811:818-849
982	sushi	Sushi domain (SCR repeat)	0.28	12.5	3	1-38:43-104:272-332
982	TNFR_c6	TNFR/NGFR cysteine-rich region	0.74	9.6	1	563-601
982	laminin_EGF	Laminin EGF-like (Domains III and V)	6.6	-12.8	1	746-791
982	metalthio	Metallothionein	7.6	-11.6	1	744-804
982	HMG_CoA synt	Hydroxymethylglutaryl-coenzyme A synthase	8.7	-342.7	1	336-625
986	MHC_II_alpha	Class II histocompatibility antigen, alpha	8.8e-13	55.9	1	37-106
986	lg	Immunoglobulin domain	8e-05	29.5	1	122-186
987	LRR	Leucine Rich Repeat	2.6e-12	54.3	4	68-91:92-114:115-137:138-159
987	UVR	UvrB/uvrC motif	5.3	-1.5	1	453-486
990	UVR	UvrB/uvrC motif	3.8	-0.3	1	552-588
991	CK_II_beta	Casein kinase II regulatory subunit	4.5e-69	242.9	1	5-124
994	RNA_pol_B	RNA polymerase beta subunit	0	1199.4	1	26-1010
994	PHD	PHD-finger	5.9	-17.0	1	1013-1048
995	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.9e-05	30.2	1	10-59
995	zf-B_box	B-box zinc finger	0.0022	24.7	1	92-134
996	HLH	Helix-loop-helix DNA-binding domain	2e-07	38.1	1	276-327
997	ras	Ras family	3.3e-12	2.0	1	23-145
998	pkinase	Protein kinase domain	3.1e-08	-16.4	1	1-139
1000	lg	Immunoglobulin domain	2.7e-06	34.4	2	42-95:225-281
1001	Y_phosphatase	Protein-tyrosine phosphatase	4.2	-86.2	1	180-409
1002	PX	PX domain	5.8e-19	76.4	1	22-138
1002	Peptidase S21	Assemblin (Peptidase family S21)	8.9	-173.6	1	76-352
1003	Y_phosph	Protein-tyrosine phosphatase	1.1	-79.3	1	98-327

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	atase					
1004	Y_phosphatase	Protein-tyrosine phosphatase	4.2	-86.2	1	180-409
1008	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	5.2	-165.9	1	64-311
1010	filament	Intermediate filament protein	1.7	-190.5	1	331-647
1010	Tektin	Tektin family	1.8	-228.5	1	192-507
1010	bZIP	bZIP transcription factor	4.4	-3.7	1	253-317
1010	spectrin	Spectrin repeat	5.6	-18.0	1	320-429
1010	SART-1	SART-1 family	8	-362.0	1	54-675
1010	Myosin_tail	Myosin tail	9.8	-555.1	1	6-734
1013	Defensin_propep	Defensin propeptide	1.2e-26	102.0	1	45-97
1013	defensins	Mammalian defensin	7.3e-14	59.5	1	110-138
1014	filament	Intermediate filament protein	0.69	-180.5	1	314-579
1014	PolyA_poly1	Poly A polymerase family	2.5	-64.5	1	348-463
1014	ERM	Ezrin/radixin/moesin family	8.7	-223.3	1	226-487
1014	Transposase_12	Transposase	9.4	-152.0	1	155-465
1015	zf-C2H2	Zinc finger, C2H2 type	1.2e-55	198.2	13	129-152:349-371:379-401:407-429:446-468:474-496:505-527:533-556:562-585:903-925:931-953:959-981:987-1010
1015	60s_ribosomal	60s Acidic ribosomal protein	0.23	-21.0	1	61-194
1015	TFIIS	Transcription factor S-II (TFIIS)	0.82	2.1	1	446-484
1015	rubredoxin	Rubredoxin	2.8	-8.3	1	900-943
1015	zf-BED	BED zinc finger	9	-7.0	1	972-1011
1021	SSF	Sodium:solute symporter family	1.7e-05	-65.8	1	5-184
1028	zf-C2H2	Zinc finger, C2H2 type	4.3e-30	113.4	5	100-122:132-154:160-182:188-210:216-238
1028	KRAB	KRAB box	7.1e-24	92.8	1	4-44
1028	zf-BED	BED zinc finger	0.63	3.4	1	78-123
1029	fn3	Fibronectin type III domain	1.8e-13	58.2	1	146-231
1029	ig	Immunoglobulin domain	0.0013	25.5	1	275-335
1031	polyprenyl_synt	Polyprenyl synthetase	0.013	-82.6	1	119-332
1032	Defensin_propep	Defensin propeptide	1.2e-26	102.0	1	68-120
1032	defensins	Mammalian defensin	7.3e-14	59.5	1	133-161
1033	MAGE	MAGE family	3.8e-34	126.8	1	1-208

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						663:669- 691:697- 719:753- 775:781- 803:809- 831:837- 859:865- 887:893- 915
1084	CBM_1	Fungal cellulose binding domain	2.6	4.4	1	38-66
1084	LIM	LIM domain	3	-15.7	1	783-847
1084	zf-BED	BED zinc finger	5.9	-5.3	2	205- 244:737- 776
1085	Band_7	SPFH domain / Band 7 family	8.1e-42	152.3	1	39-214
1087	TPR	TPR Domain	4.5e-16	66.8	2	58-91:92- 125
1090	WH1	WH1 domain	0.0017	11.6	1	11-119
1091	zf-DHHC	DHHC zinc finger domain	0.033	-11.5	1	120-158
1094	Calx-beta	Calx-beta domain	0.19	-11.6	1	23-117
1095	zf-C2H2	Zinc finger, C2H2 type	5.4e-82	285.8	12	288- 311:337- 359:365- 387:393- 415:421- 443:449- 471:477- 499:505- 527:533- 555:561- 583:589- 611:617- 639
1095	SCAN	SCAN domain	1.5e-54	194.6	1	46-141
1095	zf-BED	BED zinc finger	3.3	-3.0	2	434- 472:574- 612
1097	7tm_2	7 transmembrane receptor (Secretin family)	6.8e-21	82.8	1	325-580
1097	GPS	Latrophilin/CL-1-like GPS domain	9.5e-13	55.8	1	273-323
1097	Srg	C.elegans Srg family integral membrane prote	4.5	-217.5	1	309-565
1099	lectin_c	Lectin C-type domain	0.0011	7.2	1	6-100
1100	PDZ	PDZ domain (Also known as DHR or GLGF)	0.0014	25.3	1	12-91
1100	Tymo_45 kd_70kd	Tymovirus 45/70Kd protein	1.8	-283.9	1	1-398
1101	cadherin	Cadherin domain	8.9e-95	328.3	5	64- 156:170- 265:279- 381:394- 485:498- 595
1101	Cadherin_ C term	Cadherin cytoplasmic region	4.7e-80	279.4	1	643-794
1103	COesteras e	Carboxylesterase	0.98	-265.9	1	31-265
1104	DSPc	Dual specificity phosphatase, catalytic	9.7e-30	112.2	1	133-315

SEQ ID	Model	Description	E-value	Score	Repeats	Position
		doma				
1105	cfhand	EF hand	3.1e-21	84.0	3	124-152:160-188:208-236
1108	zf-C2H2	Zinc finger, C2H2 type	3.5e-68	239.9	10	189-212:240-262:268-290:296-319:325-347:353-375:382-404:909-931:937-960:966-988
1108	SET	SET domain	0.0012	-18.9	1	37-175
1108	zf-BED	BED zinc finger	0.1	10.4	2	276-320:922-961
1108	FYVE	FYVE zinc finger	6.8	-24.6	1	262-364
1109	Nucleoside transporter	Na <sup>+</sup> dependent nucleoside transporter	2.5e-187	635.7	1	198-613
1109	TLC	TLC ATP/ADP transporter	5.6	-382.0	1	95-407
1109	ATP-synth A	ATP synthase A chain	6.5	-79.5	1	365-503
1110	PHD	PHD-finger	5.2	-16.5	1	77-120
1113	Peptidase C48	Ulp1 protease family, C-terminal catalytic	6.5e-34	126.1	1	254-415
1114	ras	Ras family	5.5e-31	116.4	1	54-222
1114	arf	ADP-ribosylation factor family	0.0054	-80.3	1	37-213
1115	SPRY	SPRY domain	7.3e-10	46.2	1	281-419
1115	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00076	26.2	1	88-134
1116	LRR	Leucine Rich Repeat	2.1e-05	31.4	6	37-64:65-92:93-120:121-142:175-198:255-278
1117	RasGAP	GTPase-activator protein for Ras-like GTPase	6.4e-28	106.2	1	268-440
1117	PH	PH domain	0.28	15.7	1	7-78
1117	C2	C2 domain	1.9	-9.5	1	91-171
1117	bZIP	bZIP transcription factor	9	-6.7	1	997-1054
1118	COX3	Cytochrome c oxidase subunit III	1.7	-228.9	1	77-195
1118	sugar transporter	Sugar (and other) transporter	2.2	-179.3	1	32-413
1120	LMWPc	Low molecular weight phosphotyrosine protein	9.7e-56	198.6	1	7-138
1122	M	M protein repeat	6.6	13.1	2	148-168:216-236
1123	lectin_c	Lectin C-type domain	4.3e-11	50.3	1	579-646
1123	Tropomyosin	Tropomyosin	0.17	-90.1	1	304-500
1123	filament	Intermediate filament protein	0.17	-164.6	1	287-537
1123	spectrin	Spectrin repeat	5.8	-18.2	1	422-523
1127	vwa	von Willebrand factor type A domain	4.1e-63	223.1	1	252-450
1127	trypsin	Trypsin	2.1e-43	157.6	1	463-734

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1127	sushi	Sushi domain (SCR repeat)	2.4e-24	94.3	3	37-85:86-140:147-200
1128	Neur_chan_memb	Neurotransmitter-gated ion-channel tra	1e-88	308.2	1	84-334
1128	oxidored_q1_N	NADH-Ubiquinone oxidoreductase	7	-14.7	1	123-183
1129	C4	C-terminal tandem repeated domain in type 4	1.4e-148	507.0	2	477-584:585-699
1129	Collagen	Collagen triple helix repeat (20 copies)	1.9e-60	214.3	7	20-78:84-142:143-202:205-265:266-325:329-388:405-464
1132	filament	Intermediate filament protein	2.1	-193.2	1	90-330
1132	Tropomyosin	Tropomyosin	7.7	-119.0	1	151-353
1135	zf-C2H2	Zinc finger, C2H2 type	8.3e-26	99.2	5	278-303:312-339:345-369:375-399:405-429
1136	Ribosomal_S2	Ribosomal protein S2	1.7e-78	274.2	1	34-198
1137	ATP-synt_ab_N	ATP synthase alpha/beta family, beta-ba	5.2e-26	99.8	1	63-129
1139	ATP-synt_ab	ATP synthase alpha/beta family, nucleot	3.1e-06	-33.1	1	71-183
1139	ATP-synt_ab_N	ATP synthase alpha/beta family, beta-ba	0.015	14.4	1	10-68
1140	ATP-synt_ab_N	ATP synthase alpha/beta family, beta-ba	5.2e-26	99.8	1	63-129
1140	ATP-synt_ab	ATP synthase alpha/beta family, nucleot	2.6e-06	-31.8	1	132-261
1141	ank	Ankyrin repeat	6.7e-34	126.0	3	463-495:496-528:529-561
1141	BRCT	BRCA1 C Terminus (BRCT) domain	1.5e-15	65.1	2	578-689:705-812
1141	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.083	9.7	1	86-122
1143	GTP_EFTU	Elongation factor Tu GTP binding domain	0.031	-59.5	1	68-140
1145	RF-1	Peptidyl-tRNA hydrolase domain	3.3e-05	10.5	1	46-159
1146	RF-1	Peptidyl-tRNA hydrolase domain	6.4	-51.5	1	46-114
1148	WD40	WD domain, G-beta repeat	6.9e-07	36.3	1	44-80
1149	Band 41	FERM domain (Band 4.1 family)	1.1e-77	271.5	1	45-235
1150	Metallothionein_PEC	Plant PEC family metallothionein	5	-38.3	1	90-139
1153	pkinase	Protein kinase domain	1.7e-90	314.1	1	43-299

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1155	SCP	SCP-like extracellular protein	6.2e-14	56.1	1	28-200
1156	ras	Ras family	1.5e-15	40.0	1	5-98
1159	6PF2K	6-phosphofructo-2-kinase	5.2e-152	518.4	1	26-249
1159	PGAM	Phosphoglycerate mutase family	6e-100	345.5	1	250-435
1160	zf-C2H2	Zinc finger, C2H2 type	1.3e-104	361.0	13	223-245:251-273:279-301:307-329:335-357:363-385:391-413:419-441:447-469:475-497:501-523:529-551:557-579
1160	PHD	PHD-finger	0.55	-7.5	1	448-509
1160	zf-BED	BED zinc finger	1.4	0.3	2	264-302:542-580
1160	DnaJ_CX XCXGX G	DnaJ central domain (4 repeats)	2.9	-45.3	1	509-572
1160	LIM	LIM domain	7.7	-19.2	1	477-539
1160	TFIIS	Transcription factor S-II (TFIIS)	7.9	-6.3	1	450-485
1162	Patatin	Patatin-like phospholipase	0.00033	-0.6	1	1-171
1163	pkinase	Protein kinase domain	2.3e-94	326.9	1	53-303
1163	RIO1	RIO1/ZK632.3/MJ0444 family	0.37	-100.2	1	47-245
1164	Oxysterol _BP	Oxysterol-binding protein	3.8e-47	170.0	1	173-571
1166	OATP_C	Organic Anion Transporter Polypeptide (OATP)	9.9e-195	660.3	1	68-443
1166	OATP_N	Organic Anion Transporter Polypeptide (OATP)	1e-67	238.4	1	520-680
1166	7tm_5	7TM chemoreceptor	6.1	-167.4	1	184-503
1166	sugar_tr	Sugar (and other) transporter	7.8	-195.1	1	48-570
1167	pentaxin	Pentaxin family	2.3e-07	-7.3	1	25-98
1168	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.7e-05	31.7	1	537-574
1169	Peptidase M1	Peptidase family M1	4e-156	532.1	1	69-458
1170	ig	Immunoglobulin domain	0.0016	25.1	1	30-109
1172	BTB	BTB/POZ domain	8.7e-33	122.4	1	104-214
1173	F-box	F-box domain	0.0019	24.9	1	16-64
1174	TPR	TPR Domain	4.5	9.3	1	301-334
1175	2OG- FeII_Oxy	2OG-Fe(II) oxygenase superfamily	1.6e-06	35.1	1	527-648
1175	TPR	TPR Domain	4.5	9.3	1	301-334
1176	2OG- FeII_Oxy	2OG-Fe(II) oxygenase superfamily	1.6e-06	35.1	1	557-678
1177	Na_Ca_E x	Sodium/calcium exchanger protein	1.1e-23	92.1	1	236-381
1179	lactamase B	Metallo-beta-lactamase superfamily	0.059	-4.5	1	13-212
1180	fibrinogen C	Fibrinogen beta and gamma chains, C-term	1.6e-32	121.5	1	207-416

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1181	MIF	Macrophage migration inhibitory factor (MIF)	7.6e-67	235.5	1	2-115
1182	SSH	Sodium:solute symporter family	1.7e-234	792.4	1	69-503
1182	xan_ur_pe rmease	Permease family	4.3	-193.8	1	143-514
1182	PNTB	NAD(P) transhydrogenase beta subunit	5	-389.7	1	33-325
1182	60KD_IM P	60Kd inner membrane protein	6.2	-129.6	1	113-241
1182	oxidored_ ql	NADH-Ubiquinone/plastoquinone	7.4	-169.1	1	87-298
1183	Cation_ef flux	Cation efflux family	2.3e-58	207.3	1	73-311
1185	AAA	ATPase family associated with various cel	4e-89	309.5	2	236- 421:500- 620
1185	HypB_Ur eG	HypB/UreG nucleotide-binding domain	3.2	-65.8	1	234-337
1185	ArsA_AT Pase	Anion-transporting ATPase	8.5	-195.7	1	234-482
1186	HCO3_co transp	HCO3- transporter family	0	1389.6	1	141-1023
1186	xan_ur_pe rmease	Permease family	0.33	-164.5	1	518-985
1187	homeobox	Homeobox domain	2.4e-16	67.7	1	51-107
1188	efhand	EF hand	6.7	9.0	1	13-41
1191	GST_C	Glutathione S-transferase, C-terminal domain	0.93	0.3	1	134-326
1194	PPR	PPR repeat	0.0019	24.9	1	14-48
1195	thioered	Thioredoxin	0.018	-13.7	1	390-497
1197	ENV_pol yprotein	ENV polyprotein (coat polyprotein)	1.2e-08	-24.1	1	86-529
1200	UQ_con	Ubiquitin-conjugating enzyme	1.3e-23	91.9	1	60-190
1202	7tm_1	7 transmembrane receptor (rhodopsin family)	2.1e-23	91.2	1	59-306
1202	7tm_5	7TM chemoreceptor	4.3	-164.7	1	37-314
1203	7tm_1	7 transmembrane receptor (rhodopsin family)	5.9e-37	136.2	1	59-341
1203	7tm_5	7TM chemoreceptor	2.2	-159.4	1	37-338
1204	SH3	SH3 domain	2.5e-05	31.1	1	257-317
1204	UBA	UBA/TS-N domain	0.00013	28.8	1	36-76
1204	PGAM	Phosphoglycerate mutase family	0.00044	-75.5	1	438-625
1205	heme_1	Heme/Steroid binding domain	0.00053	19.5	1	37-112
1207	transmem brane4	Tetraspanin family	0.29	-69.8	1	11-110
1208	OATP_C	Organic Anion Transporter Polypeptide	1.3e- 135	464.0	1	148-524
1208	kazal	Kazal-type serine protease inhibitor d	0.11	4.9	1	555-601
1208	sugar_tr	Sugar (and other) transporter	0.15	-145.7	1	128-626
1208	lig_chan	Ligand-gated ion channel	3.3	-153.6	1	193-524
1208	7tm_1	7 transmembrane receptor	4.2	-115.5	1	177-473
1208	Cytidylylt rans	Phosphatidate cytidylyltransferase	4.6	-87.5	1	177-268
1215	thyroglob ulin_1	Thyroglobulin type-1 repeat	3.2e-35	130.4	2	90- 153:216- 281
1215	kazal	Kazal-type serine protease inhibitor	7.5e-09	42.8	1	40-84
1215	efhand	EF hand	0.057	20.0	2	351-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						379:388-416
1216	annexin	Annexin	7e-61	215.7	2	72-139:144-211
1217	annexin	Annexin	2.2e-86	300.4	3	44-111:116-183:199-267
1218	annexin	Annexin	7e-61	215.7	2	44-111:116-183
1219	Armadillo_seg	Armadillo/beta-catenin-like repeat	5.3e-30	113.1	5	351-393:405-447:448-498:499-541:543-585
1219	GA	GA module	8.3	-5.7	1	180-224
1221	p450	Cytochrome P450	1e-122	421.1	1	30-483
1222	p450	Cytochrome P450	1.7e-06	-35.8	1	30-328
1223	A2M_N	Alpha-2-macroglobulin family N-terminal regi	4.3e-12	-71.6	1	1-468
1225	Thymosin	Thymosin beta-4 family	2.3e-16	67.8	1	2-41
1227	WD40	WD domain, G-beta repeat	1.6e-37	138.1	7	115-151:165-201:207-244:250-286:293-328:334-370:391-431
1236	F-box	F-box domain	5e-07	36.8	1	210-258
1236	UvrD-helicase	UvrD/REP helicase	0.00011	-157.2	1	441-920
1237	LRR	Leucine Rich Repeat	2.3e-25	97.7	8	42-65:66-88:89-111:112-134:135-157:158-180:181-203:204-227
1238	TPR	TPR Domain	9.6e-54	192.0	10	22-55:56-86:87-120:121-154:155-188:189-222:223-255:290-323:328-361:362-395
1241	cadherin	Cadherin domain	0.00011	29.0	2	48-151:165-254
1243	TTL	Tubulin-tyrosine ligase family	3.6e-31	117.0	1	1-225
1245	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	4.2e-08	40.4	1	190-221



SEQ ID	Model	Description	E-value	Score	Repeats	Position
1245	zf-UBP	Zn-finger in ubiquitin-hydrolases and other	1.2e-05	32.2	1	62-148
1246	ank	Ankyrin repeat	3.8e-92	319.5	11	12-44:45-77:79-110:112-142:145-177:179-211:212-244:245-277:278-310:312-344:345-374
1250	CIq	CIq domain	0.00033	-3.8	1	827-946
1250	filament	Intermediate filament protein	1.3	-187.6	1	360-645
1250	spectrin	Spectrin repeat	1.9	-12.5	1	492-591
1250	TNF	TNF(Tumor Necrosis Factor) family	4.1	-20.5	1	835-946
1250	Apolipoprotein	Apolipoprotein A1/A4/E family	5.7	-113.3	1	200-469
1250	sigma70	Sigma-70 factor	9	-116.2	1	462-650
1252	laminin_Nterm	Laminin N-terminal (Domain VI)	3.2e-52	186.9	1	1-223
1252	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-38	141.0	3	225-292:295-355:358-409
1252	NTR	NTR/C345C module	7.2e-30	112.6	1	479-591
1252	Keratin_B2	Keratin, high sulfur B2 protein	6.7	-81.2	1	318-451
1253	enolase	Enol-ase	0.038	-162.0	1	11-136
1256	HIT	HIT family	1.5e-55	198.0	1	51-162
1257	ank	Ankyrin repeat	5.9e-24	93.0	4	39-67:68-100:101-133:134-164
1258	lectin_c	Lectin C-type domain	1.3e-21	85.2	1	51-181
1258	lectin_c	Lectin C-type domain	1.3e-21	85.2	1	51-181
1262	mito_carr	Mitochondrial carrier protein	8.7e-67	235.3	3	7-100:102-221:224-319
1263	serpin	Serpin (serine protease inhibitor)	8.7e-109	374.8	1	87-463
1264	MHC_I	Class I Histocompatibility antigen, domains	1.3e-141	483.9	1	25-203
1265	MHC_I	Class I Histocompatibility antigen, domains	2.3e-130	446.5	1	25-203
1266	MHC_I	Class I Histocompatibility antigen, domains	2.7e-117	403.1	1	22-187
1267	MHC_I	Class I Histocompatibility antigen, domains	1.1e-115	397.7	1	25-196
1268	MHC_I	Class I Histocompatibility antigen, domains	2.9e-118	406.3	1	25-196
1268	ig	Immunoglobulin domain	9.5e-08	39.2	1	221-286
1269	MHC_I	Class I Histocompatibility antigen, domains	4.2e-132	452.3	1	25-204
1271	MHC_I	Class I Histocompatibility antigen, domains	1e-144	494.2	1	25-203
1272	MHC_I	Class I Histocompatibility antigen,	2.8e-95	329.9	1	25-204

SEQ ID	Model	Description	E-value	Score	Repeats	Position
		domains				
1273	MHC_I	Class I Histocompatibility antigen, domains	3.3e-140	479.2	1	25-203
1274	Kelch	Kelch motif	1.4e-91	117.7	6	271-316:318-366:368-413:415-460:462-507:509-554
1274	BTB	BTB/POZ domain	3.1e-38	140.4	1	23-130
1275	IQ	IQ calmodulin-binding motif	0.0037	23.9	1	394-414
1276	Glycos_tr ansf 2	Glycosyl transferase	2.2e-22	87.8	1	126-308
1276	Ricin_B_I ectin	QXW lectin repeat	0.0045	23.7	2	478-518:520-557
1280	ig	Immunoglobulin domain	3.4e-05	30.7	2	62-145:174-240
1281	UCH-1	Ubiquitin carboxyl-terminal hydrolases famII	1.5e-12	55.1	1	100-131
1285	UBX	UBX domain	2.9e-22	87.4	1	205-284
1286	UBX	UBX domain	2.9e-22	87.4	1	251-330
1287	DnaJ	DnaJ domain	9e-38	138.9	1	8-70
1288	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.9e-09	42.8	1	9-57
1288	zf-B_box	B-box zinc finger	1.8e-06	34.9	1	177-217
1288	SPRY	SPRY domain	0.0016	14.8	1	479-605
1288	zf-UBR1	Putative zinc finger in N-recogin	2.2	-18.4	1	180-237
1289	PKD	PKD domain	0	1026.8	16	293-372:397-483:485-568:572-677:679-763:765-846:849-931:933-1017:1019-1099:1101-1183:1185-1269:1271-1353:1355-1438:1440-1522:1524-1612:1614-1696
1289	REJ	REJ domain	2.3e-290	978.0	1	1723-2248
1289	PLAT	PLAT/LH2 domain	2.6e-25	97.5	1	2673-2789
1289	GPS	Latrophilin/CL-1-like GPS domain	1.1e-15	65.5	1	2566-2615
1289	lectin_c	Lectin C-type domain	0.59	-23.7	1	2-87
1289	DUF26	Domain of unknown function DUF26	7.8	-16.5	1	2220-2262
1290	CNH	CNH domain	2.7e-24	94.2	1	69-375
1292	RhoGAP	RhoGAP domain	1.8e-59	211.0	1	125-279
1293	Peptidase_M10	Matrixin	8.2e-110	378.2	1	48-211
1293	fn2	Fibronectin type II domain	3.5e-84	293.1	3	230-271:288-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						329:347-388
1293	hemopexin	Hemopexin	1e-33	125.5	3	486-530:608-654:656-699
1294	Peptidase M10	Matrixin	8.2e-110	378.2	1	48-211
1294	fn2	Fibronectin type II domain	3.5e-84	293.1	3	230-271:288-329:347-388
1297	UQ_con	Ubiquitin-conjugating enzyme	3.3e-20	80.6	1	400-557
1297	TT_ORF2	TT viral ORF2	3.6	-92.9	1	546-667
1297	UQ_con	Ubiquitin-conjugating enzyme	3.3e-20	80.6	1	400-557
1297	TT_ORF2	TT viral ORF2	3.6	-92.9	1	546-667
1298	ig	Immunoglobulin domain	2.9e-236	798.3	21	25-84:119-177:245-303:339-397:432-490:524-583:618-676:709-768:801-859:894-954:990-1048:1121-1179:1217-1275:1382-1440:1477-1535:1569-1627:1664-1722:1756-1816:1851-1911:1947-2005:2040-2098
1298	Adeno_E3_CRI	Adenovirus E3 region protein CRI	0.062	-3.7	1	1212-1288
1299	cNMP_binding	Cyclic nucleotide-binding domain	6.2e-28	106.2	1	363-459
1299	ion_trans	Ion transport protein	8.9e-21	82.5	1	69-265
1299	ATP-synt_DE	ATP synthase, Delta/Epsilon chain, long	6.8	6.0	1	478-525
1301	RGS	Regulator of G protein signaling domain	1.6e-49	177.9	1	56-172
1302	THF_DH_G_CYH_C	Tetrahydrofolate dehydrogenase/cyclohyd	1e-99	344.7	1	60-235
1303	gln-synt	Glutamine synthetase	1.3e-179	610.1	1	1-321
1304	gln-synt	Glutamine synthetase	0.13	-214.4	1	1-95
1305	SCAN	SCAN domain	7.5e-61	215.6	1	42-137
1306	Methyltransferase_5	MraW methylase family	4.6e-06	-96.4	1	70-205
1307	ion_trans	Ion transport protein	8.3e-18	72.6	1	438-672
1307	ank	Ankyrin repeat	1.9e-06	34.8	2	77-108:163-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						195
1307	Srg	C.elegans Srg family integral membrane prot	8.1	-222.4	1	418-669
1310	Ammonium transporter	Ammonium Transporter Family	1.9e-56	200.9	1	25-429
1310	FecCD	FecCD transport family	0.89	-200.6	1	97-331
1311	Kelch	Kelch motif	2.6e-60	213.8	6	311-359:361-411:413-458:460-505:507-556:559-606
1311	BTB	BTB/POZ domain	1.6e-28	108.1	1	23-181
1313	zf-B_box	B-box zinc finger	9.6e-30	112.2	2	92-133:418-459
1313	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.3e-23	91.8	2	15-59:341-385
1313	SPRY	SPRY domain	3.2e-23	90.6	1	672-813
1313	PHD	PHD-finger	0.97	-9.8	1	14-62
1313	NB-ARC	NB-ARC domain	9.5	-151.3	1	48-311
1313	zf-UBR1	Putative zinc finger in N-recognin	9.8	-24.7	1	421-470
1314	SRCR	Scavenger receptor cysteine-rich domain	1.7e-25	98.1	1	37-133
1315	adh_short	short chain dehydrogenase	5.8e-33	122.9	1	38-293
1317	ANP	Atrial natriuretic peptide	1.2e-51	185.0	1	43-150
1318	EGF	EGF-like domain	3.6e-26	100.4	6	512-547:553-591:597-634:640-675:747-781:787-827
1318	ig	Immunoglobulin domain	2.1e-06	34.7	1	170-227
1318	TIL	Trypsin Inhibitor like cysteine rich dom	1.9	-6.8	1	741-787
1318	ldl_recept_a	Low-density lipoprotein receptor domain	6.6	-8.8	1	551-593
1318	TILa	TILa domain	6.9	-8.5	1	733-792
1321	FKBP	FKBP-type peptidyl-prolyl cis-trans isomeras	5.7e-45	162.8	1	234-336
1322	PX	PX domain	1.1e-25	98.8	1	273-382
1322	SH3	SH3 domain	6.5e-12	53.0	1	3-59
1323	ras	Ras family	5.2e-16	45.4	1	35-218
1323	GTP_EFTU	Elongation factor Tu GTP binding domain	0.53	-76.1	1	31-223
1323	MobB	Molybdopterin guanine dinucleotide synthesis	4.8	-45.8	1	36-150
1323	GTP_CD C	Cell division protein	5.7	-217.6	1	36-247
1324	pkinase	Protein kinase domain	4.6e-51	183.1	1	199-527
1325	pkinase	Protein kinase domain	4.6e-51	183.1	1	199-527
1327	Peptidase C1	Papain family cysteine protease	7.3e-110	378.4	1	73-349
1328	Peptidase C1	Papain family cysteine protease	7.3e-110	378.4	1	114-390
1330	ig	Immunoglobulin domain	4.6e-07	36.9	2	52-108:145-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						201
1332	Sec7	Sec7 domain	1.3e-71	251.3	1	345-536
1332	PH	PH domain	0.25	16.2	1	567-676
1332	IQ	IQ calmodulin-binding motif	0.35	17.4	1	13-33
1333	cadherin	Cadherin domain	1.6e-94	327.4	5	68-159:173-268:282-386:399-490:503-600
1333	Cadherin_C term	Cadherin cytoplasmic region	1.6e-76	267.6	1	648-819
1335	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	7.5e-35	129.2	1	5-133
1336	SH3	SH3 domain	2.4e-10	47.8	1	495-549
1336	PID	Phosphotyrosine interaction domain (PTB/PID)	0.29	-13.3	1	52-181
1336	SAM_PN T	Sterile alpha motif (SAM)/Pointed domain	6	-25.0	1	608-687
1336	SH2	SH2 domain	8.6	-25.5	1	268-347
1338	UCH-2	Ubiquitin carboxyl-terminal hydrolase	1.5e-20	81.7	1	350-411
1338	UCH-1	Ubiquitin carboxyl-terminal hydrolases	1.1e-12	55.5	1	111-142
1338	TFIIA	Transcription factor IIA, alpha/beta s	1.7	-151.4	1	386-698
1338	Tymo_45 kd_70kd	Tymovirus 45/70Kd protein	3.3	-291.1	1	310-647
1338	MARCKS	MARCKS family	6.8	-95.6	1	573-865
1340	RCC1	Regulator of chromosome condensation (RCC1)	5.6e-10	46.6	6	77-136:140-192:195-245:248-298:301-356:359-406
1342	Peptidase M1	Peptidase family M1	4.6	-194.5	1	159-470
1342	ubiquitin	Ubiquitin family	5.4	-4.4	1	538-616
1345	crystall	Beta/Gamma crystallin	3.3e-38	140.4	2	1-53:61-144
1345	WD40	WD domain, G-beta repeat	6.7e-09	43.0	1	269-305
1348	AAA	ATPase family associated with various cellul	0.97	-33.9	1	131-307
1349	AAA	ATPase family associated with various cellul	0.97	-33.9	1	131-307
1351	PHD	PHD-finger	6.3e-15	63.0	1	190-237
1351	PHD	PHD-finger	6.3e-15	63.0	1	190-237
1353	CUB	CUB domain	3.3e-13	57.3	1	416-524
1353	sushi	Sushi domain (SCR repeat)	1.5e-05	31.9	1	357-412
1355	SPRY	SPRY domain	3.4e-19	77.2	1	396-519
1355	fn3	Fibronectin type III domain	1e-08	42.4	1	259-345
1355	zf-B box	B-box zinc finger	8.9e-07	35.9	1	44-86
1356	Patatin	Patatin-like phospholipase	0.59	-42.1	1	10-118
1358	ELM2	ELM2 domain	3.2e-21	84.0	1	195-256
1358	myb_DN A-binding	Myb-like DNA-binding domain	1.1e-09	45.6	1	299-345
1359	Reprolysin	Reprolysin (M12B) family zinc metallo	1.4e-12	55.3	1	239-457
1359	Pep_M12 B_propep	Reprolysin family propeptide	3.6e-12	53.9	1	90-216

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1359	tsp_1	Thrombospondin type 1 domain	3.4e-07	37.4	5	551-601:829-884:888-944:946-1002:1007-1057
1359	EB	EB module	8.4	-11.7	1	452-531
1363	ank	Ankyrin repeat	6.2e-26	99.6	5	72-104:105-137:138-170:180-212:222-255
1366	C2	C2 domain	1e-75	264.9	2	161-247:293-381
1367	C2	C2 domain	1e-75	264.9	2	161-247:293-381
1368	p450	Cytochrome P450	5e-110	378.9	1	47-502
1370	aa_permeases	Amino acid permease	1.3e-08	-108.1	1	49-452
1370	Neur_channel_memb	Neurotransmitter-gated ion-channel tr	0.37	-96.5	1	330-585
1370	ion_trans	Ion transport protein	1.4	-2.3	1	288-615
1370	Transp_cyt_pur	Permease for cytosine/purines, uracil	1.5	-178.6	1	47-442
1370	Aa_trans	Transmembrane amino acid transporter	1.9	-190.3	1	67-409
1370	DUF140	Domain of unknown function DUF140	2.6	-156.6	1	109-312
1370	Nucleoside_trans	Nucleoside transporter	3.2	-154.9	1	357-658
1370	xan_ur_permease	Permease family	4.1	-193.2	1	56-429
1370	DUF6	Integral membrane protein DUF6	7.1	-22.4	1	536-671
1370	NADHdh	NADH dehydrogenase	7.3	-213.9	1	212-616
1370	SNF	Sodium:neurotransmitter symporter fam	9.2	-458.6	1	117-450
1372	kinesin	Kinesin motor domain	2.1e-135	463.2	1	53-341
1372	Translin	Translin family	10	-82.4	1	315-462
1373	LRR	Leucine Rich Repeat	1.9e-27	104.6	7	60-83:84-107:108-131:132-155:157-180:181-204:205-225
1373	ig	Immunoglobulin domain	1.2e-05	32.1	1	310-368
1373	LRRCT	Leucine rich repeat C-terminal domain	4.7e-05	30.2	1	249-294
1373	fn3	Fibronectin type III domain	7.1e-05	29.6	1	425-505
1373	LRRNT	Leucine rich repeat N-terminal domain	0.83	13.7	1	27-58
1374	kinesin	Kinesin motor domain	9.5e-14	1.2	1	1-131
1375	zf-DHHC	DHHC zinc finger domain	9.1e-34	125.6	1	101-165
1376	EGF	EGF-like domain	3.2e-45	163.6	9	49-84:90-126:132-167:177-213:217-252:286-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						321:327- 362:368- 401:407- 442
1376	CUB	CUB domain	9.6e-18	72.4	1	809-918
1376	TIL	Trypsin Inhibitor like cysteine rich domain	0.73	-2.0	1	84-132
1376	Keratin_B2	Keratin, high sulfur B2 protein	0.9	-67.6	1	111-242
1376	granulin	Granulin	1.1	-12.1	1	285-323
1376	metalthio	Metallothionein	5.9	-10.3	1	363-431
1376	DUF141	Domain of unknown function DUF141	6.7	-15.1	1	799-922
1380	ion trans	Ion transport protein	0.066	16.8	1	153-318
1380	ABC2_membrane	ABC-2 type transporter	6.1	-130.1	1	145-334
1380	oxidored_q1	NADH-Ubiquinone/plastoquinone	6.2	-167.5	1	46-317
1380	OATP_C	Organic Anion Transporter Polypeptide	9.5	-236.4	1	75-316
1381	pkinase	Protein kinase domain	9.7e-80	278.3	1	205-486
1384	ig	Immunoglobulin domain	0.00034	27.4	1	65-142
1388	LRR	Leucine Rich Repeat	4.9e-16	66.7	4	20-43:44- 67:68- 91:92-115
1388	LRRCT	Leucine rich repeat C-terminal domain	7.4e-09	42.9	1	125-175
1388	GPS	Latrophilin/CL-I-like GPS domain	0.0041	20.8	1	641-693
1388	HRM	Hormone receptor domain	0.0076	16.3	1	285-354
1388	7tm_2	7 transmembrane receptor (Secretin family)	0.01	-96.0	1	704-981
1388	ig	Immunoglobulin domain	3.3	10.9	1	196-265
1389	MACPF	MAC/Perforin domain	0.016	-71.3	1	30-313
1391	HD	HD domain	8.3e-07	36.1	1	32-127
1392	efhand	EF hand	1.5e-05	31.8	2	1-25:33-61
1394	MORN	MORN repeat	1.1e-32	122.1	7	39-61:62- 85:86- 108:109- 131:132- 154:155- 177:178- 200
1395	MORN	MORN repeat	3.1e-31	117.2	6	39-61:62- 85:86- 108:143- 165:166- 188:189- 211
1396	EPH_lbd	Ephrin receptor ligand binding domain	4.6e-135	462.1	1	31-204
1396	pkinase	Protein kinase domain	8e-74	258.7	1	635-892
1396	fn3	Fibronectin type III domain	2.5e-31	117.5	2	329- 425:437- 524
1396	SAM	SAM domain (Sterile alpha motif)	2.5e-21	84.3	1	928-992
1396	PHD	PHD-finger	3.7	-15.1	1	259-296
1397	Exo_endo_phos_fa	Endonuclease/Exonuclease/phosphatase	0.34	-11.2	1	357-643
1397	sugar_tr	Sugar (and other) transporter	8.8	-196.7	1	7-343
1397	Exo_endo_phos_fa	Endonuclease/Exonuclease/phosphatase	0.34	-11.2	1	357-643

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1397	sugar_tr	Sugar (and other) transporter	8.8	-196.7	1	7-343
1401	homeobox	Homeobox domain	0.097	-3.3	1	78-126
1403	Tropomyosin	Tropomyosin	2.4	-110.1	1	341-547
1403	filament	Intermediate filament protein	2.6	-195.5	1	412-760
1403	UvrD-helicase	UvrD/REP helicase	8	-249.4	1	153-720
1403	Myosin_tail	Myosin tail	8.9	-551.2	1	20-777
1404	C1q	C1q domain	0.00033	-3.8	1	827-946
1404	filament	Intermediate filament protein	1.3	-187.6	1	360-645
1404	spectrin	Spectrin repeat	1.9	-12.5	1	492-591
1404	TNF	TNF(Tumor Necrosis Factor) family	4.1	-20.5	1	835-946
1404	Apolipoprotein	Apolipoprotein A1/A4/E family	5.7	-113.3	1	200-469
1404	sigma70	Sigma-70 factor	9	-116.2	1	462-650
1405	Cache	Cache domain	6.5e-12	53.0	2	402-481:721-813
1406	ASC	Amiloride-sensitive sodium channel	2e-125	430.1	1	159-579
1407	pkinase	Protein kinase domain	0.22	-115.5	1	5-217
1408	PBP	Phosphatidylethanolamine-binding protein	1.8e-71	250.9	1	1-167
1410	abhydrolase	alpha/beta hydrolase fold	1.4	-12.1	1	75-318
1412	rrm	RNA recognition motif.	2.7e-12	54.3	3	259-329:360-433:477-550
1414	DEP	Domain found in Dishevelled, Egl-10, and Plc	3.5e-32	120.3	2	173-247:275-349
1414	PH	PH domain	1e-09	45.7	1	29-144
1414	PDZ	PDZ domain (Also known as DHR or GLGF)	0.013	18.7	2	375-456:460-531
1418	SCAN	SCAN domain	2.6e-51	183.9	1	36-131
1418	zf-C2H2	Zinc finger, C2H2 type	4.6e-25	96.7	5	406-428:435-457:463-485:522-545:553-575
1418	KRAB	KRAB box	0.023	14.2	1	220-260
1418	zf-BED	BED zinc finger	10	-7.4	1	438-486
1419	EGF	EGF-like domain	5.1e-28	106.5	9	13-40:45-72:77-104:109-136:141-168:173-200:205-232:237-264:269-296
1419	Keratin_B2	Keratin, high sulfur B2 protein	1.2	-69.3	1	100-251
1419	Gamma-thionin	Gamma-thionins family	4.8	-8.7	1	124-163



SEQ ID	Model	Description	E-value	Score	Repeats	Position
1421	Ferric_reduct	Ferric reductase like transmembrane	2.8e-64	227.0	1	63-564
1421	NAD_binding	Oxidoreductase NAD-binding domain	4	-34.1	1	381-551
1421	FAD_binding_6	Oxidoreductase FAD-binding domain	5	-28.7	1	245-335
1421	rubredoxin	Rubredoxin	6.9	-11.0	1	409-436
1422	zf-C2H2	Zinc finger, C2H2 type	5e-12	53.4	2	1057-1079:1085-1109
1422	zf-TRAF	TRAF-type zinc finger	5	-6.6	1	1056-1101
1422	Tymo_45kd_70kd	Tymovirus 45/70Kd protein	6	-298.2	1	343-700
1422	zf-BED	BED zinc finger	7.1	-6.0	1	1070-1110
1423	7tm_5	7TM chemoreceptor	3.3	-162.5	1	181-451
1423	Cytidyltransferase	Phosphatidate cytidyltransferase	5	-87.9	1	21-135
1424	CAP_GLY	CAP-Gly domain	7.2e-46	165.8	2	196-238:398-440
1424	ank	Ankyrin repeat	9.2e-09	42.5	3	1-40:42-76:79-111
1425	PAP2	PAP2 superfamily	1.5e-08	41.8	1	166-313
1426	SCAN	SCAN domain	6.2e-70	245.7	1	33-128
1426	zf-C2H2	Zinc finger, C2H2 type	1.5e-44	161.4	6	239-261:267-289:295-317:323-345:351-373:379-401
1426	zf-BED	BED zinc finger	0.67	3.1	1	280-318
1426	DCI	DCI domain	5.1	3.6	1	295-338
1426	zf-C4	Zinc finger, C4 type (two domains)	9.7	-55.1	1	323-364
1427	xan_ur_permease	Permease family	7.1	-199.5	1	104-453
1428	LRR	Leucine Rich Repeat	2.3e-16	67.8	4	80-103:104-127:128-151:152-175
1428	LRRCT	Leucine rich repeat C-terminal domain	0.00079	26.2	1	185-234
1431	PH	PH domain	7.6e-15	62.8	1	19-117
1432	PH	PH domain	6.4e-21	82.9	1	55-153
1434	filament	Intermediate filament protein	2.9	-196.8	1	128-488
1434	K-box	K-box region	4.1	-38.4	1	277-357
1434	OspD	Borrelia outer surface protein D	5.3	-69.3	1	151-409
1434	Apolipoprotein	Apolipoprotein A1/A4/E family	5.7	-113.3	1	56-318
1437	RhoGAP	RhoGAP domain	5.7e-57	202.7	1	1152-1305
1437	PH	PH domain	3.5e-18	73.8	1	922-1030
1437	PDZ	PDZ domain (Also known as DHR or GLGF)	0.0013	25.4	1	28-128
1441	annexin	Annexin	4.1e-109	375.9	4	18-79:80-135:151-219:227-294

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1443	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0075	18.7	1	1256-1307
1443	PHD	PHD-finger	0.18	-2.9	1	1255-1310
1443	WD40	WD domain, G-beta repeat	2.9	13.4	1	189-225
1443	K_tetra	K+ channel tetramerisation domain	3.5	-39.5	1	830-916
1443	Clathrin	Region in Clathrin and VPS	8.9	-25.2	1	976-1129
1444	R11a	Regulatory subunit of type II PKA R-s	0.31	10.8	1	17-54
1444	Alpha_adaptin_C	Alpha adaptin AP2, C-terminal domain	7	-63.6	1	91-155
1445	TK	Thymidine kinase	3.4e-98	339.6	1	61-231
1446	GDPD	Glycerophosphoryl diester phosphodies	5.4e-08	40.0	1	154-403
1446	Glycosyltransferase_4	Glycosyl transferase	4.9	-87.4	1	22-145
1447	adh_short	short chain dehydrogenase	0.98	-91.8	1	2-196
1448	K-box	K-box region	0.64	-28.5	1	61-126
1449	PHD	PHD-finger	0.01	8.4	1	1-42
1452	rrm	RNA recognition motif.	4.5e-19	76.8	1	77-148
1454	rvt	Reverse transcriptase	3.6e-34	126.9	1	385-570
1454	Gag_MA	Matrix protein (MA), p15	0.0018	-21.0	1	10-131
1454	Gag_p30	Gag P30 core shell protein	0.54	-80.3	1	211-390
1458	COX5A	Cytochrome c oxidase subunit Va	1.2e-55	198.3	1	42-131
1459	Guanylate_kinase	Guanylate kinase	6.2e-38	139.4	1	515-624
1459	PDZ	PDZ domain (Also known as DHR or GLGF)	6.8e-11	49.6	1	256-335
1459	SH3	SH3 domain	0.027	5.9	1	348-415
1459	L27	L27 domain	0.049	20.1	1	186-238
1459	Caulimovirus_mov	Caulimovirus movement protein	7.1	-185.3	1	420-673
1459	A_deaminase	Adenosine/AMP deaminase	7.8	-138.5	1	64-421
1461	hexokinase	Hexokinase	4.3e-284	957.2	1	53-499
1463	Occludin	Occludin/ELL family	6.3	-249.1	1	33-394
1464	trypsin	Trypsin	4.7e-72	252.8	1	30-232
1466	DDHD	DDHD domain	8.6e-117	401.4	1	613-860
1466	DUF203	Domain of unknown function	8.7	-69.8	1	254-460
1467	Glycosyltransferase_1	Glycosyl transferases group 1	1.8e-27	104.7	1	286-470
1468	EMP24_GP25L	emp24/gp25L/p24 family	3.5e-70	246.6	1	5-183
1469	EMP24_GP25L	emp24/gp25L/p24 family	3.5e-81	283.1	1	5-208
1470	14-3-3	14-3-3 protein	2.2e-142	486.5	1	5-249
1471	filament	Intermediate filament protein	0.53	-177.6	1	2-249
1471	spectrin	Spectrin repeat	7.1	-19.1	1	34-130
1472	MtN3_slv	MtN3/saliva family	5.4	-31.6	1	35-139
1472	ATP-synth_A	ATP synthase A chain	7.4	-80.2	1	91-214
1474	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	4.3e-07	37.0	2	531-557;663-688
1474	zf-C2H2	Zinc finger, C2H2 type	6.3	11.3	2	205-229;618-642
1475	SpoU_methylase	SpoU rRNA Methylase family	2.1e-27	104.5	1	145-301

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1476	filament	Intermediate filament protein	2.4	-194.5	1	427-720
1476	Tropomyosin	Tropomyosin	3	-111.7	1	539-761
1476	spectrin	Spectrin repeat	3.3	-15.3	1	427-526
1476	K-box	K-box region	7.1	-41.3	1	248-335
1476	Borrelia_orfA	Borrelia ORF-A	9.8	-102.9	1	440-736
1477	MMR_HS_R1	GTPase of unknown function	1.5e-90	314.2	1	178-521
1477	DUF258	Protein of unknown function, DUF258	9.6	-84.6	1	343-465
1479	RNase_PH	3' exoribonuclease family	1.2e-96	334.5	2	48-251:358-581
1479	S1	S1 RNA binding domain	0.057	19.9	1	675-750
1479	KH-domain	KH domain	0.35	9.3	1	609-651
1482	COLF1	Fibrillar collagen C-terminal domain	5.8e-29	109.6	1	97-277
1482	Collagen	Collagen triple helix repeat (20 copies)	8.5e-05	29.4	1	2-61
1483	COLF1	Fibrillar collagen C-terminal domain	1.6e-35	131.4	1	110-293
1483	Collagen	Collagen triple helix repeat (20 copies)	8.5e-05	29.4	1	2-61
1484	CH	Calponin homology (CH) domain	5.6e-14	59.9	1	4-104
1485	MoaE	MoaE protein	7	-55.7	1	21-96
1486	zf-C2H2	Zinc finger, C2H2 type	6.8	10.9	2	871-896:904-929
1487	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.6	-3.3	1	336-377
1489	FH2	Formin Homology 2 Domain	0.00017	-49.7	1	3-329
1490	AAA	ATPase family associated with various	4e-45	163.3	1	370-565
1490	SKI	Shikimate kinase	0.068	-52.5	1	369-506
1490	Viral_helicase1	Viral (Superfamily 1) RNA helicase	1.8	-67.0	1	371-563
1490	LON	ATP-dependent protease La (LON) domain	3.6	-69.4	1	12-220
1491	Tropomodulin	Tropomodulin	4.1e-78	272.9	1	34-402
1491	WH2	WH2 motif	0.83	16.1	1	534-553
1491	pkinase	Protein kinase domain	5.9	-136.0	1	334-538
1494	xan_ur_permease	Permease family	2.9	-189.3	1	72-377
1494	Na_sulph_symp	Sodium:sulfate symporter transmembran	5.3	-356.1	1	212-541
1494	Glycosyltransferase_4	Glycosyl transferase	7.3	-90.3	1	374-528
1494	STE3	Pheromone A receptor	7.5	-203.9	1	314-603
1494	DUF221	Domain of unknown function DUF221	9.6	-234.2	1	196-576
1494	7tm_5	7TM chemoreceptor	9.7	-171.0	1	122-365
1494	oxidored_q1	NADH-Ubiquinone/plastoquinone	9.7	-171.5	1	42-264
1495	lectin_c	Lectin C-type domain	4.7e-34	126.6	1	53-164
1496	Cytochrome_b561	Cytochrome b561	2.1e-113	390.2	1	1-240
1498	Hydrolase	haloacid dehalogenase-like hydrolase	0.0045	16.9	1	31-443
1498	Cation_ATPase_C	Cation transporting ATPase, C-terminu	0.26	-25.8	1	535-706
1498	oxidored_q4	NADH-ubiquinone/plastoquinone oxidore	4.4	-34.0	1	631-705
1499	DEAD	DEAD/DEAH box helicase	3e-64	226.9	1	139-356
1499	helicase	Helicase conserved C-terminal domain	4.1e-32	120.1	1	447-518

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	C					
1502	C2	C2 domain	1.3e-51	184.9	2	28-109:184-264
1503	ank	Ankyrin repeat	1.6e-31	118.2	6	743-775:776-807:808-840:842-874:875-915:916-948
1504	ank	Ankyrin repeat	1.4e-167	570.1	16	57-89:90-122:123-155:210-242:243-275:276-308:363-398:399-431:432-464:525-557:558-590:591-623:644-675:678-710:711-743:744-776
1504	SAM	SAM domain (Sterile alpha motif)	1.3e-09	45.4	1	872-934
1504	PARP	Poly(ADP-ribose) polymerase catalytic domain	0.022	-59.4	1	954-1161
1504	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomerase	1.3	-204.0	1	208-536
1505	PHD	PHD-finger	0.26	-4.5	1	132-191
1505	DC1	DC1 domain	2.8	5.8	1	131-159
1506	PHD	PHD-finger	0.26	-4.5	1	156-215
1506	DC1	DC1 domain	2.8	5.8	1	155-183
1507	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.6e-08	40.6	1	224-261
1507	LON	ATP-dependent protease La (LON) domain	0.007	-21.6	1	305-510
1507	TPR	TPR Domain	1.6	13.6	2	41-74:75-108
1508	ig	Immunoglobulin domain	1e-76	268.3	12	78-131:171-245:276-330:364-432:463-516:552-623:654-705:740-797:828-880:914-981:1012-1067:1101-1169
1512	FYVE	FYVE zinc finger	3.2e-14	60.7	1	152-261
1512	HypA	Hydrogenase expression/synthesis hypA	0.81	-51.2	1	97-194
1512	RNA_POL_M_15K	RNA polymerases M/15 Kd subunit	2.1	-1.7	1	160-212

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	D					
1516	Gelsolin	Gelsolin repeat	0.76	5.9	1	1011-1052
1518	V1R	Vomeronal organ pheromone receptor family	2.3e-11	41.1	1	73-338
1518	7tm_1	7 transmembrane receptor (rhodopsin family)	0.044	-69.7	1	62-325
1520	SPRY	SPRY domain	5.2e-24	93.2	1	95-230
1521	Tropomodulin	Tropomodulin	0.065	-128.4	1	214-495
1521	LRR	Leucine Rich Repeat	1.8	15.0	4	348-371:376-403:404-427:432-456
1522	zf-CCHC	Zinc knuckle	0.051	15.9	1	13-30
1523	Skp1	Skp1 family	6.3e-10	46.4	1	17-80
1524	RhoGAP	RhoGAP domain	4.2e-31	116.8	1	125-285
1525	UQ_con	Ubiquitin-conjugating enzyme	1.4e-39	144.9	1	1-126
1527	LRR	Leucine Rich Repeat	1.6e-35	131.4	9	86-109:110-133:134-157:158-181:182-205:206-229:230-251:254-277:279-302
1527	LRRNT	Leucine rich repeat N-terminal domain	6.6e-06	33.1	1	33-60
1527	LRRCT	Leucine rich repeat C-terminal domain	0.048	17.9	1	312-362
1528	K_tetra	K+ channel tetramerisation domain	0.0016	-5.0	1	117-220
1529	MORN	MORN repeat	1.8e-24	94.7	7	1049-1071:1072-1094:1100-1122:1123-1143:1151-1171:1198-1220:1221-1244
1529	VPS9	Vacuolar sorting protein 9 (VPS9) domain	8.3e-06	32.7	1	1551-1656
1529	RCC1	Regulator of chromosome condensation (RCC1)	8.5e-06	32.7	3	168-216:527-574:579-625
1529	RhoGEF	RhoGEF domain	0.097	-40.8	1	694-884
1529	PH	PH domain	0.23	16.5	1	901-1005
1530	profilin	Profilin	1.4e-63	224.6	1	3-135
1531	profilin	Profilin	7.4e-48	172.4	1	3-119
1532	60s_ribosomal	60s Acidic ribosomal protein	3.3	-34.2	1	39-153
1533	jmjC	jmjC domain	0.01	-0.1	1	1-50
1533	PHD	PHD-finger	0.042	2.9	2	508-549:609-655
1534	kinesin	Kinesin motor domain	3.5e-64	226.7	1	1-177
1536	aminotran 3	Aminotransferase class-III	7.8e-42	152.4	1	1-373

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1536	LEA	Late embryogenesis abundant protein	5.6	-4.7	1	109-177
1539	Hydrolase	haloacid dehalogenase-like hydrolase	0.0064	15.3	1	264-685
1539	Cation_A TPase_C	Cation transporting ATPase, C-terminu	4.6	-46.1	1	784-916
1541	TPR	TPR Domain	0.00036	27.3	2	135- 168:204- 237
1542	PCMT	Protein-L-isoaspartate(D-aspartate) O- methyl	1.2e-11	21.8	1	9-224
1543	Peptidase C54	Peptidase family C54	3.1e-58	206.9	1	76-364
1545	homeobox	Homeobox domain	4.8e-26	100.0	1	233-286
1546	zf-C2H2	Zinc finger, C2H2 type	3.1e-85	296.6	14	14:36:42- 64:70- 92:99- 122:128- 150:163- 185:199- 221:227- 249:255- 277:283- 305:311- 333:339- 361:367- 389:395- 417
1546	TFIIS	Transcription factor S-II (TFIIS)	1.9	-1.0	1	202-237
1546	zf-BED	BED zinc finger	2.3	-1.7	1	324-362
1546	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.6	-5.4	1	341-372
1547	Ribosoma l S5	Ribosomal protein S5	3.4e-09	44.0	1	222-352
1548	IQ	IQ calmodulin-binding motif	1e-24	95.5	5	748- 768:771- 791:794- 814:935- 955:958- 978
1552	DUF6	Integral membrane protein DUF6	0.14	6.6	1	150-279
1552	SBF	Sodium Bile acid symporter family	9.2	-75.2	1	143-321
1553	zf-C2H2	Zinc finger, C2H2 type	2.1e-05	31.4	3	80- 105:107- 130:144- 169
1554	F-box	F-box domain	7.7e-05	29.5	1	4-52
1555	Ran_BP1	RanBP1 domain	1.1e-88	308.0	1	37-161
1555	WH1	WH1 domain	6.8	-26.8	1	45-159
1556	actin	Actin	8.4e- 151	514.4	1	1-372
1557	GTP_EFT U	Elongation factor Tu GTP binding doma	9.7	-93.3	1	91-355
1557	Defensin_ propep	Defensin propeptide	9.8	-11.4	1	1-50
1559	GTP_EFT U	Elongation factor Tu GTP binding domain	1.5e-11	51.8	1	125-348
1559	GTP_EFT U_D3	Elongation factor Tu C-terminal domain	8.1e-07	33.1	1	451-541
1559	GTP_EFT U_D2	Elongation factor Tu domain 2	1e-06	35.8	1	363-446

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1559	ATP-bind	Conserved hypothetical ATP binding protei	8.5	-132.9	1	126-312
1559	dynamin	Dynamain family	8.7	-85.0	1	110-278
1567	carb_anhy drase	Eukaryotic-type carbonic anhydrase	4.6e-170	578.4	1	5-241
1568	Animal perox idase	Animal haem peroxidase	8.1e-164	557.6	1	144-683
1568	DUF37	Domain of unknown function DUF37	6.5	-36.0	1	462-518
1569	DAO	FAD dependent oxidoreductase	0.055	-90.8	1	49-381
1571	CH	Calponin homology (CH) domain	1.4e-25	98.4	1	126-233
1573	NUDIX	MutT-like domain	5.5e-12	53.3	1	96-221
1574	HECT	HECT-domain (ubiquitin-transferase)	4.3e-16	66.9	1	281-573
1575	ig	Immunoglobulin domain	2.8	11.5	1	122-187
1577	7tm_1	7 transmembrane receptor	3.4	-113.2	1	42-246
1577	Bac_rhod opsin	Bacteriorhodopsin	9.6	-139.9	1	111-313
1578	fn3	Fibronectin type III domain	0.21	11.2	1	121-211
1579	Acetyltran sf	Acetyltransferase (GNAT) family	2.4e-14	61.1	1	548-624
1580	Acetyltran sf	Acetyltransferase (GNAT) family	2.4e-14	61.1	1	653-729
1580	Acetyltran sf	Acetyltransferase (GNAT) family	2.4e-14	61.1	1	653-729
1582	GIDA	Glucose inhibited division protein A	0.0017	-414.5	1	68-196
1583	efhand	EF hand	1.2	14.9	1	23-51
1585	Dynein_h eavy	Dynein heavy chain	3.6e-18	-92.1	1	1-363
1587	Sm	Sm protein	2e-07	38.1	1	43-124
1588	PDZ	PDZ domain (Also known as DHR or GLGF)	3.1e-15	64.1	1	3-83
1590	MAP1_L C3	Microtubule associated protein 1A/1B, light	0.04	-35.1	1	99-187
1591	Syntaxin	Syntaxin	2.3e-09	38.1	1	1-266
1591	synaptobr evin	Synaptobrevin	5.8	-14.5	1	184-272
1591	DUF148	Domain of unknown function DUF148	7.7	-38.1	1	17-129
1592	laminin_E GF	Laminin EGF-like (Domains III and V)	1.2	-4.2	1	153-196
1592	EGF	EGF-like domain	2.4	10.9	3	140-177;284-313;351-380
1592	metalthio	Metallothioncin	4.8	-9.3	1	288-348
1593	DnaJ	DnaJ domain	3.4e-40	146.9	1	3-69
1594	HMG_bo x	HMG (high mobility group) box	2.6e-27	104.1	1	346-414
1598	HMG_bo x	HMG (high mobility group) box	3.4e-30	113.8	1	45-113
1600	CUB	CUB domain	6.9	-43.0	1	224-313
1601	DUF6	Integral membrane protein DUF6	1.1e-12	55.6	2	113-238;266-390
1601	sugar_tr	Sugar (and other) transporter	5.7	-191.4	1	55-405
1601	oxidored_ q1	NADH-Ubiquinone/plastoquinone (complex I)	6	-167.3	1	131-389
1602	FF	FF domain	2.3e-33	124.3	5	272-321;339-388;406-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						461:486-541:622-673
1602	WW	WW domain	4.3e-20	80.2	2	88-117:129-158
1603	FF	FF domain	2.3e-33	124.3	5	235-284:302-351:369-424:449-504:585-636
1603	WW	WW domain	1.1e-09	45.6	1	92-121
1605	AT_hook	AT hook motif	1.9	11.9	1	360-372
1606	aminotran 5	Aminotransferase class-V	1.3e-127	437.3	1	37-377
1607	aminotran 5	Aminotransferase class-V	3.5e-94	326.3	1	37-331
1611	Granin	Granin (chromogranin or secretogranin)	6.6	-185.2	1	125-609
1612	PHD	PHD-finger	0.59	-7.8	1	551-610
1613	Branch	Core-2/I-Branching enzyme	1e-77	271.6	1	46-313
1614	mbt	mbt repeat	3.2e-101	349.7	4	78-153:192-265:304-381:412-486
1614	SAM_PN T	Sterile alpha motif (SAM)/Pointed domain	0.0021	6.9	1	809-888
1614	SAM	SAM domain (Sterile alpha motif)	0.023	20.6	1	822-885
1615	UPF0103	Protein of unknown function DUF52	4.7e-64	226.2	1	9-270
1616	C2	C2 domain	6.8e-36	132.7	2	606-695:755-842
1617	C2	C2 domain	7.8e-35	129.2	2	87-176:236-323
1618	C2	C2 domain	0.16	2.4	1	265-346
1619	7tm_1	7 transmembrane receptor (rhodopsin family)	3.9e-20	80.3	1	217-427
1620	K_tetra	K+ channel tetramerisation domain	1.1e-25	98.7	1	3-101
1620	BTB	BTB/POZ domain	9	-22.4	1	21-104
1623	cyclin	Cyclin, N-terminal domain	0.057	-1.4	1	46-149
1624	zf-C2H2	Zinc finger, C2H2 type	8.9e-19	75.8	4	34-57:71-93:112-134:143-165
1627	PDZ	PDZ domain (Also known as DHR or GLGF)	4.2e-16	66.9	1	66-149
1628	MttA_Hcf 106	mttA/Hcf106 family	2.5	-14.8	1	54-107
1628	Tropomyo sin	Tropomyosin	4	-114.1	1	74-272
1628	Syntaxin	Syntaxin	5.7	-103.5	1	82-402
1628	PI3_PI4_ kinase	Phosphatidylinositol 3- and 4-kinase	8.5	-118.0	1	125-342
1628	HlyD	HlyD family secretion protein	9.4	-64.2	1	129-400
1628	UPF0089	Uncharacterised protein family	10	-132.7	1	150-338
1629	rrm	RNA recognition motif.	1.7e-47	171.2	2	72-



SEQ ID	Model	Description	E-value	Score	Repeats	Position
						142:156-226
1632	Ribosomal L10	Ribosomal protein L10	4.2	-31.6	1	70-173
1632	Ribosomal L10	Ribosomal protein L10	4.2	-31.6	1	70-173
1635	death	Death domain	1.5	2.0	1	261-348
1636	death	Death domain	1.5	2.0	1	73-160
1637	Gelsolin	Gelsolin repeat	4.1e-92	319.4	6	27-76:148-188:265-307:398-451:523-564:626-668
1639	TBC	TBC domain	2e-08	15.3	1	98-293
1640	TBC	TBC domain	2e-07	1.3	1	98-297
1641	homeobox	Homeobox domain	0.0097	7.0	1	83-135
1646	transmembrane4	Tetraspanin family	1.6e-75	264.3	1	18-264
1652	LacY_symport	LacY proton/sugar symporter	4.9	-335.5	1	66-299
1652	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	7.6	-169.3	1	53-279
1653	Colipase_C	Colipase, C-terminal domain	4.3e-24	93.5	1	21-65
1654	SH2	SH2 domain	0.0091	3.5	1	1-83
1658	SUI1	Translation Initiation factor SUI1	4.4e-46	166.5	1	50-149
1661	jmjC	jmjC domain	0.00052	13.9	1	308-415
1663	SH3	SH3 domain	0.011	9.5	1	332-388
1664	UBA	UBA/TS-N domain	6.7e-06	33.0	1	194-233
1664	TUDOR	Tudor domain	0.2	-0.7	1	506-627
1665	Ribosomal S21	Ribosomal protein S21	0.0039	11.7	1	10-62
1666	transmembrane4	Tetraspanin family	2.2e-71	250.6	1	23-264
1669	RuBisCO_small	Ribulose biphosphate carboxylase, small	2.8	-52.1	1	354-430
1671	LRR	Leucine Rich Repeat	2e-50	180.9	12	29-47:48-71:72-95:96-118:119-142:143-166:167-189:190-213:214-235:236-259:260-283:284-307
1671	7tm_1	7 transmembrane receptor	0.0032	-43.2	1	439-688
1671	Cytidyltransferase	Phosphatidate cytidyltransferase	7.1	-89.9	1	520-617
1671	oxidored_q1	NADH-Ubiquinone/plastoquinone	9.7	-171.5	1	475-685
1671	MerC	MerC mercury resistance protein	9.8	-87.5	1	534-632
1672	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	4e-28	106.9	1	292-364
1672	UCH-1	Ubiquitin carboxyl-terminal hydrolases	1.9e-14	61.4	1	35-66

SEQ ID	Model	Description	E-value	Score	Repeats	Position
		famil				
1673	F-box	F-box domain	0.00071	26.3	1	87-134
1674	Lamp	Lysosome-associated membrane glycoprotein	5.7	191.1	1	351-653
1675	FGGY	FGGY family of carbohydrate kinases, N-termi	2.7e-45	193.9	1	20-282
1675	FGGY_C	FGGY family of carbohydrate kinases, C-termi	5.5e-23	89.8	1	285-491
1676	Keratin_B 2	Keratin, high sulfur B2 protein	7.4	-81.9	1	24-201
1678	S_100	S-100/ICaBP type calcium binding domain	8.3	-9.6	1	909-941
1680	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	7.4e-24	92.7	1	12-369
1681	WD40	WD domain, G-beta repeat	9.3e-14	59.1	6	305-343:352-389:395-432:440-476:487-524:583-621
1683	Ribosomal L44	Ribosomal protein L44	1e-38	142.1	1	17-95
1686	WD40	WD domain, G-beta repeat	8.9e-14	59.2	2	8-43:50-86
1688	FliE	Flagellar hook-basal body complex protein Fl	5.1	-27.5	1	673-763
1690	dCMP_cyt deam	Cytidine and deoxycytidylate deaminase	2e-13	58.0	1	12-100
1691	G-gamma	GGL domain	5.1	-8.6	1	712-760
1692	cpn60_TCP1	TCP-1/cpn60 chaperonin family	0.012	-260.5	1	32-187
1693	Glycophorin A	Glycophorin A	4.4	-43.1	1	16-149
1696	zf-C2H2	Zinc finger, C2H2 type	4.5e-15	63.5	6	92-115:120-143:174-198:210-233:329-353:363-386
1698	LRR	Leucine Rich Repeat	0.44	17.0	4	37-58:59-80:81-102:103-125
1699	VHS	VHS domain	9.5e-60	211.9	1	5-146
1700	rrm	RNA recognition motif.	3.6e-23	90.4	3	128-203:332-402:413-480
1701	ank	Ankyrin repeat	3.8e-101	349.4	12	12-44:45-77:79-111:112-144:145-177:179-211:212-244:245-277:278-310:312-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						344:345- 374:375- 407
1701	URO-D	Uroporphyrinogen decarboxylase (URO-D)	7.8	-229.7	1	79-354
1702	pkinase	Protein kinase domain	0.00012	-68.0	1	31-278
1702	HEAT	HEAT repeat	1.2	15.6	2	342- 380:499- 537
1705	cyclin	Cyclin, N-terminal domain	3.8e-11	50.5	1	157-279
1708	WD40	WD domain, G-beta repeat	1.5e-11	51.8	5	278- 313:371- 407:413- 447:493- 529:535- 569
1709	SH2	SH2 domain	0.002	10.0	1	287-364
1710	abhydrolase	alpha/beta hydrolase fold	2.2e-20	81.2	1	124-355
1710	abhydrolase_2	Phospholipase/Carboxylesterase	1.2	-84.9	1	179-359
1711	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.002	23.7	1	280-320
1711	PHD	PHD-finger	1.9	-12.4	1	282-323
1712	WD40	WD domain, G-beta repeat	3.2e-18	74.0	5	67- 101:123- 157:164- 199:209- 246:253- 290
1714	Acyltransferase	Acyltransferase	0.0011	14.0	1	83-217
1719	helicase_C	Helicase conserved C-terminal domain	1.2e-19	78.7	1	397-475
1719	DEAD	DEAD/DEAH box helicase	4.6e-07	10.4	1	2-210
1719	IPT	Isopentenyl transferase	7.9	-160.7	1	17-172
1720	Na_Ca_Ex	Sodium/calcium exchanger protein	8e-76	265.3	2	109- 249:471- 616
1720	DUF205	Domain of unknown function DUF	5.3	-112.7	1	85-253
1720	Fumarate_red_D	Fumarate reductase subunit D	8.4	-49.5	1	518-620
1721	vwa	von Willebrand factor type A domain	9.6e-29	108.9	1	34-205
1721	fn3	Fibronectin type III domain	3e-15	64.1	2	212- 287:332- 413
1724	pkinase	Protein kinase domain	1.6e-06	-41.3	1	40-359
1725	BRCT	BRCA1 C Terminus (BRCT) domain	1e-15	65.6	3	3-93:642- 730:753- 833
1727	BRCT	BRCA1 C Terminus (BRCT) domain	7.2	1.2	1	45-130
1728	rrm	RNA recognition motif	1.1e-05	32.4	2	545- 612:880- 942
1728	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.012	22.2	1	285-311
1728	PWI	PWI domain	0.047	-0.6	1	6-78
1730	PX	PX domain	2.5e-31	117.5	1	94-211
1731	PMP22_C claudin	PMP-22/EMP/MP20/Claudin family	1.5e-56	201.3	1	1-157

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1733	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1733	Vac_Fusion	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1733	CUT	CUT domain	8.5	-38.0	1	159-240
1734	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1734	Vac_Fusion	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1734	CUT	CUT domain	8.5	-38.0	1	159-240
1738	efhand	EF hand	1.5e-16	68.4	2	40-68:76-104
1742	trypsin	Trypsin	6.5	-55.6	1	33-255
1743	Exonuclease	Exonuclease	1.2e-36	135.2	1	39-213
1745	Smr	Smr domain	0.0029	13.0	1	1594-1672
1745	RyR	RyR domain	1.5	-29.0	1	1312-1403
1745	L27	L27 domain	3.6	5.1	1	1573-1626
1746	Smr	Smr domain	0.0029	13.0	1	1611-1689
1746	RyR	RyR domain	1.5	-29.0	1	1312-1403
1746	L27	L27 domain	3.6	5.1	1	1590-1643
1746	Smg4_UPF3	Smg-4/UPF3 family	9.7	-74.5	1	1379-1518
1747	mito_carr	Mitochondrial carrier protein	1.3e-81	284.5	3	1-90:98-198:200-288
1748	OSCP	ATP synthase delta (OSCP) subunit	8.4	-94.4	1	67-213
1749	Oxysterol_BP	Oxysterol-binding protein	3.4e-78	273.2	1	488-875
1749	PH	PH domain	2.2e-09	44.6	1	52-146
1750	lactamase_B	Metallo-beta-lactamase superfamily	4.1	-28.9	1	1-153
1751	lipoxxygenase	Lipoxygenase	9.5e-133	454.4	1	126-703
1751	PLAT	PLAT/LH2 domain	1.6e-33	124.8	1	2-116
1753	Rho_GDI	RHO protein GDP dissociation inhibitor	3.2e-113	389.5	1	1-187
1756	GRAM	GRAM domain	7.5e-17	69.4	1	110-177
1757	homeobox	Homeobox domain	3.6e-29	110.3	1	21-77
1758	lipocalin	Lipocalin / cytosolic fatty-acid binding protein	1.1e-24	95.4	1	38-168
1759	ig	Immunoglobulin domain	3.1e-13	57.4	2	35-112:160-234
1761	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	0.078	-128.7	1	16-259
1761	DUF250	Domain of unknown function, DUF250	0.45	-85.1	1	162-337
1761	DUF6	Integral membrane protein DUF6	2.5	-14.8	1	192-328
1761	secY	eubacterial secY protein	7.2	-246.6	1	36-243
1761	FecCD	FecCD transport family	9.8	-221.2	1	120-328
1762	Keratin_B2	Keratin, high sulfur B2 protein	3.3e-07	32.9	2	11-113:114-204
1763	sugar_tr	Sugar (and other) transporter	0.018	-119.2	1	43-449
1763	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	4.7	-165.1	1	146-442
1765	VPS9	Vacuolar sorting protein 9 (VPS9) domain	4.5e-33	123.3	1	380-484
1765	RA	Ras association (RalGDS/AF-6) domain	0.73	-5.9	1	518-607

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1766	SSF	Sodium:solute symporter family	5.9e-206	697.6	1	106-535
1766	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	4.8	-165.2	1	216-521
1766	MIP	Major intrinsic protein	5.8	-121.9	1	112-364
1766	DsbD	Cytochrome C biogenesis protein transmemb	8.6	-97.3	1	195-425
1767	Peptidase_M3	Peptidase family M3	1.3e-203	689.8	1	251-701
1768	RasGAP	GTPase-activator protein for Ras-like	1.3e-26	101.9	1	449-621
1768	PH	PH domain	0.012	22.2	1	112-236
1768	C2	C2 domain	2.6	-10.9	1	249-332
1768	Tymo_45 kd_70kd	Tymovirus 45/70Kd protein	4.2	-293.9	1	561-979
1768	RNA_pol	DNA-dependent RNA polymerase	5.1	-234.7	1	381-1225
1768	PHD	PHD-finger	6.9	-17.6	1	214-273
1770	rrm	RNA recognition motif.	0.48	5.6	2	238-323:352-422
1772	zf-C2H2	Zinc finger, C2H2 type	1.6e-87	304.2	13	49-71:197-219:225-247:253-275:281-303:309-331:337-359:365-387:393-415:421-443:449-471:477-499:505-527
1772	zf-BED	BED zinc finger	8.9	-6.9	1	490-528
1773	ATP-synt C	ATP synthase subunit C	5.4e-08	40.0	1	62-127
1774	zf-B_box	B-box zinc finger	7.2e-14	59.5	1	90-131
1774	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	48.4	1	15-58
1774	PHD	PHD-finger	1.1	-10.3	1	14-61
1774	zf-AN1	AN1-like Zinc finger	1.4	-3.2	1	15-53
1774	zf-UBR1	Putative zinc finger in N-recognin	7.6	-23.6	1	93-146
1775	FH2	Formin Homology 2 Domain	5.4e-50	179.5	1	21-455
1775	WH2	WH2 motif	0.0058	23.3	1	441-456
1777	PHD	PHD-finger	8.7	-18.6	1	493-522
1779	Branch	Core-2/I-Branching enzyme	3.9e-05	-52.8	1	175-516
1780	TFIIS	Transcription factor S-II (TFIIS)	3.9	-3.7	1	295-344
1781	SH3	SH3 domain	1.3e-13	58.6	1	454-508
1782	filament	Intermediate filament protein	3.9	-200.0	1	134-406
1783	SET	SET domain	2e-53	190.9	1	3878-4006
1783	PHD	PHD-finger	4.7e-28	106.6	3	20-71:72-118:147-200
1783	HMG_box	HMG (high mobility group) box	0.0047	12.3	1	710-773
1783	DC1	DC1 domain	8.5	1.7	3	19-50:69-98:146-176
1784	zf-DHHC	DHHC zinc finger domain	2.4e-25	97.7	1	90-154
1785	zf-C2H2	Zinc finger, C2H2 type	9.3e-14	59.1	4	18-40:64-86:92-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						115:178-200
1788	ion_trans	Ion transport protein	8.3e-18	72.6	1	438-672
1788	ank	Ankyrin repeat	1.9e-06	34.8	2	77-108:163-195
1788	Srg	C.elegans Srg family integral membrane prot	8.1	-222.4	1	418-669
1791	ubiquitin	Ubiquitin family	0.0036	24.0	1	124-195
1792	Gag_p10	Retroviral GAG p10 protein	4e-23	90.2	1	1-89
1798	Ribosomal S12	Ribosomal protein S12	0.003	-14.2	1	7-66
1799	efhand	EF hand	1.1e-07	39.0	3	281-309:318-346:353-381
1799	Acyltransferase	Acyltransferase	0.0001	26.8	1	18-203
1801	zf-C2H2	Zinc finger, C2H2 type	3.2e-79	276.6	12	160-182:188-210:216-238:244-266:272-294:300-322:355-377:431-453:459-481:487-509:515-537:543-565
1801	LIM	LIM domain	4.7	-17.4	1	433-487
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1804	efhand	EF hand	2.5e-08	41.1	2	16-44:56-82
1806	LRR	Leucine Rich Repeat	1.5e-07	38.5	5	130-151:152-173:174-195:196-217:221-243
1807	COX3	Cytochrome c oxidase subunit III	3.5	-233.2	1	51-219
1807	CblM	CblM	9.2	-93.3	1	114-249
1807	oxidored_q5_N	NADH-ubiquinone oxidoreductase chain 4	9.8	-59.5	1	89-169
1808	Sulfotransfer	Sulfotransferase protein	6.6	-108.5	1	39-282
1814	Metallophos	Calcineurin-like phosphoesterase	0.23	14.3	1	36-241
1815	rrm	RNA recognition motif.	0.67	4.1	1	201-269
1816	filament	Intermediate filament protein	1.5	-188.9	1	1-253
1817	MAGE	MAGE family	4.2e-17	70.3	2	14-613:655-867
1817	Atrophin-1	Atrophin-1 family	9.5	-684.8	1	4-783
1818	Tropomod	Tropomodulin	8.1	-168.0	1	362-653

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	ulin					
1819	Hydrolase	haloacid dehalogenase-like hydrolase	3.4e-21	83.8	1	28-282
1820	Fe_hyd_l g_C	Iron only hydrogenase large subunit, C- te	1.3e-92	321.1	1	204-516
1820	Fe_hyd_S SU	Iron hydrogenase small subunit	8.3	-13.1	1	529-576
1821	filament	Intermediate filament protein	1e-143	490.8	1	55-366
1822	Keratin_B 2	Keratin, high sulfur B2 protein	0.082	-51.3	1	12-174
1824	metalthio	Metallothionein	5.7e-17	69.8	1	48-108
1824	AFP	Insect antifreeze protein	2.6	14.5	1	61-72
1825	C2	C2 domain	4.7e-53	189.7	2	373- 462:528- 617
1825	RPH3A_e ffector	Rabphilin-3A effector domain	0.035	-127.1	1	1-237
1825	zf-MIZ	MIZ zinc finger	0.4	-10.5	1	80-111
1825	PHD	PHD-finger	0.97	-9.7	1	62-108
1825	LIM	LIM domain	2.2	-14.6	1	80-128
1825	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1	-4.0	1	63-105
1828	efhand	EF hand	8.4e-08	39.4	3	106- 134:142- 170:407- 435
1829	60s_ribos omal	60s Acidic ribosomal protein	7.4	-38.2	1	163-291
1831	Tektin	Tektin family	1.6	-227.3	1	1-150
1833	EGF	EGF-like domain	1.1e-32	122.0	5	26-54:57- 85:92- 124:156- 187:194- 226
1833	laminin_E GF	Laminin EGF-like (Domains III and V)	1.6	-5.9	1	29-63
1833	Bowman- Birk_leg	Bowman-Birk serine protease inhibitor	4.8	-16.7	1	37-85
1833	metalthio	Metallothionein	5.5	-10.1	1	59-117
1834	7tm_1	7 transmembrane receptor (rhodopsin family)	4.8e-05	-0.8	1	31-273
1834	7tm_2	7 transmembrane receptor (Secretin family)	5.5	-151.6	1	9-248
1835	rrm	RNA recognition motif	0.05	15.7	1	75-141
1835	Met_10	Met-10+ like-protein	0.065	-100.4	1	333-583
1835	UPF0020	Putative RNA methylase family UPF0020	0.073	-53.8	1	410-566
1835	PCMT	Protein-L-isoaspartate(D-aspartate) O-	0.2	-114.1	1	391-543
1835	Methyltra nsf_4	Putative methyltransferase	2.1	-82.0	1	424-566
1835	notch	Notch (DSL) domain	6.1	-10.5	1	233-271
1836	Kelch	Kelch motif	3e-33	123.9	4	242- 288:290- 331:333- 378:380- 435
1836	BTB	BTB/POZ domain	2.3	-15.2	1	1-129
1837	tsp_1	Thrombospondin type 1 domain	0.0014	23.3	5	139- 196:203- 256:257-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						313:320-370:374-432
1837	EB	EB module	6.4	-10.5	1	330-399
1838	adh_zinc	Zinc-binding dehydrogenase	7.3e-55	195.7	1	44-369
1838	Lipase_GDSL	Lipase/Acylhydrolase with GDSL-like motif	5.5	-20.4	1	103-189
1839	pkinase	Protein kinase domain	2.4e-05	-58.0	1	81-333
1841	zf-C2H2	Zinc finger, C2H2 type	4.4e-30	113.4	7	141-163:169-191:197-219:225-247:350-372:378-400:406-434
1841	KRAB	KRAB box	5.1e-23	89.9	1	44-84
1841	TFIIS	Transcription factor S-II (TFIIS)	2.4	-1.9	1	144-179
1841	Lentiviral_Tat	Lentiviral Tat protein	4.9	-23.0	1	35-125
1841	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.2	-7.1	1	352-411
1841	rubredoxin	Rubredoxin	7.4	-11.1	1	403-433
1842	E2F_TDP	Transcription factor E2F/dimerisation partne	1.5	-95.1	1	18-229
1843	V_ATPase_sub_a	V-type ATPase 116kDa subunit family	0	1258.7	1	26-831
1843	UCR_14kD	Ubiquinol-cytochrome C reductase compl	3.2	-40.4	1	6-112
1843	Flp	Flp family	4.8	-148.9	1	533-661
1843	PsbH	Photosystem II 10 kDa phosphoprotein	7.1	5.1	1	751-803
1844	aa_permeases	Amino acid permease	5.6e-08	-125.3	1	28-529
1844	Aa_transpro	Transmembrane amino acid transporter pro	0.71	-178.9	1	30-408
1844	BPD_transport_2	Branched-chain amino acid transport syst	3.3	-116.9	1	175-440
1844	MVIN	Virulence factor MVIN	3.5	-240.9	1	87-515
1844	FecCD	FecCD transport family	5.3	-216.0	1	311-521
1844	ion_trans	Ion transport protein	6.2	-11.7	1	288-495
1844	7tm_5	7TM chemoreceptor	7.1	-168.6	1	238-498
1848	sugar_tr	Sugar (and other) transporter	0.0072	-107.9	1	12-407
1848	xan_ur_permease	Permease family	5.6	-196.7	1	38-359
1848	FecCD	FecCD transport family	6.3	-217.4	1	56-287
1848	Nucleoside_trans	Nucleoside transporter	8.1	-162.4	1	82-365
1848	Pucc	Pucc protein	9.8	-283.2	1	51-403
1849	Filamin	Filamin/ABP280 repeat	2.3e-20	81.1	1	396-494
1849	zf-B_box	B-box zinc finger	9.3e-11	49.2	2	130-176:186-227
1849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0016	24.4	1	29-62
1853	ank	Ankyrin repeat	1.1e-98	341.3	10	485-517:518-550:551-583:584-616:617-



SEQ ID	Model	Description	E-value	Score	Repeats	Position
						650:651- 683:684- 716:717- 749:750- 780:782- 814
1853	pkinaase	Protein kinase domain	1.6e-50	181.3	1	22-286
1854	ras	Ras family	1.4e-13	17.8	1	5-194
1855	Acyltransf erace	Acyltransferase	3e-34	127.2	1	92-289
1856	wap	WAP-type (Whey Acidic Protein) 'four-disulfi	0.0025	18.7	1	31-72
1857	arf	ADP-ribosylation factor family	2.5e-11	24.6	1	7-193
1857	GTP_EFT U	Elongation factor Tu GTP binding domain	1.6	-82.5	1	19-198
1858	zf-C2H2	Zinc finger, C2H2 type	2.1e-09	44.7	5	82- 104:110- 132:138- 161:364- 386:392- 416
1858	PHD	PHD-finger	7.7	-18.1	1	365-400
1859	zf-C2H2	Zinc finger, C2H2 type	7.2e-20	79.4	4	119- 141:147- 169:175- 198:214- 237
1860	BTB	BTB/POZ domain	1.7e-29	111.4	1	22-126
1860	zf-C2H2	Zinc finger, C2H2 type	5.1e-14	60.0	3	373- 395:401- 423:429- 452
1860	K_tetra	K+ channel tetramerisation domain	0.44	-30.2	1	34-124
1860	zf-BED	BED zinc finger	8.9	-6.9	1	363-396
1861	SNF2_N	SNF2 and others N-terminal domain	2.1e-72	254.0	1	137-473
1861	helicase_ C	Helicase conserved C-terminal domain	1.4e-24	95.1	1	559-632
1861	DEAD	DEAD/DEAH box helicase	0.26	-59.6	1	124-337
1861	SEC-C	SEC-C motif	0.43	13.8	1	426-446
1862	ras	Ras family	2.4e-69	243.8	1	19-217
1862	arf	ADP-ribosylation factor family	4.1e-05	-53.5	1	1-182
1864	rrm	RNA recognition motif.	0.053	15.4	1	129-191
1867	T-box	T-box	4.3e-09	29.9	1	1-92
1870	F-box	F-box domain	1.8	15.0	1	124-171
1871	PH	PH domain	1.1e-13	58.9	1	170-273
1872	isodh	Isocitrate/isopropylmalate dehydrogenase	1.4e- 123	423.9	1	10-383
1873	ank	Ankyrin repeat	1.8e-08	41.5	2	39-71:72- 104
1874	ank	Ankyrin repeat	1.8e-08	41.5	2	67-99:100- 132
1875	PAP2	PAP2 superfamily	0.0034	13.0	1	1-107
1876	DUF51	Protein of unknown function DUF51	5.7e-13	52.5	1	107-261
1877	zf-C2H2	Zinc finger, C2H2 type	1.5e-72	254.5	9	285- 307:313- 335:341- 363:369- 391:397-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						419:425- 447:451- 473:479- 501:507- 529
1877	KRAB	KRAB box	2.7e-21	84.2	1	49-89
1877	zf-BED	BED zinc finger	0.74	2.7	1	344-392
1877	TFIIS	Transcription factor S-II (TFIIS)	1.5	-0.0	1	369-407
1877	GATA	GATA zinc finger	2.1	-7.1	1	477-524
1877	LIM	LIM domain	2.5	-15.1	1	371-435
1877	E6	Early Protein (E6)	5.7	-66.7	1	315-402
1878	AAA	ATPase family associated with various	1.3e-62	221.4	1	217-409
1878	Sigma54_ activat	Sigma-54 interaction domain	4.6	-165.4	1	184-365
1879	SSF	Sodium:solute symporter family	4.8e- 170	578.3	1	58-460
1880	SSF	Sodium:solute symporter family	1.3e- 198	673.2	1	58-487
1881	perilipin	Perilipin family	6.7e-53	189.2	1	12-369
1882	aminotran _1_2	Aminotransferase class I and II	7.5e-07	25.0	1	165-515
1883	DSPc	Dual specificity phosphatase, catalytic doma	2.5e-30	114.2	1	54-199
1884	ig	Immunoglobulin domain	7.2e-14	59.5	2	34- 111:155- 229
1885	MCM	MCM2/3/5 family	4.6e-12	-67.3	1	106-391
1886	Kelch	Kelch motif	1.8e-63	224.3	6	262- 306:309- 356:358- 403:405- 453:455- 495:497- 544
1886	BTB	BTB/POZ domain	5.3e-32	119.7	1	26-134
1887	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1887	rrm	RNA recognition motif.	0.00026	27.8	1	1342-1407
1887	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1888	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1888	rrm	RNA recognition motif.	0.00026	27.8	1	1303-1368
1888	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1889	rrm	RNA recognition motif.	0.00026	27.8	1	1245-1310
1889	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	Atrophin- 1	Atrophin-1 family	6.9	-676.1	1	237-986
1890	Na_H_Ex changer	Sodium/hydrogen exchanger family	2.4e-18	74.4	1	119-520
1890	Na_Ca_E x	Sodium/calcium exchanger protein	3.1	-43.6	1	270-384
1890	7tm_5	7TM chemoreceptor	3.8	-163.7	1	259-503
1890	Abi	CAAX amino terminal protease family	5.9	-25.8	1	309-401
1890	oxidored_ ql	NADH-Ubiquinone/plastoquinone	7.9	-169.7	1	251-502
1891	Acyl- CoA_hydr o	Cytosolic long-chain acyl-CoA thioeste	8.9e-72	251.9	2	26- 168:200- 336
1891	tRNA_ant	OB-fold nucleic acid binding domain	3.5	5.8	1	230-307

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	i					
1892	zf-DHHC	DHHC zinc finger domain	8.6e-18	72.5	1	145-207
1894	SPRY	SPRY domain	4.5e-11	50.2	1	353-474
1894	fn3	Fibronectin type III domain	0.054	17.6	1	165-258
1895	dsrm	Double-stranded RNA binding motif	1.5e-12	55.1	2	229-293;337-401
1895	WW	WW domain	0.00016	28.5	1	20-49
1896	SPRY	SPRY domain	9.9e-26	98.9	1	186-301

TABLE 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
951	1e07	A	279	369	5.7e-21	0.77	1.00		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPFF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
951	1e07	A	4	98	1.7e-07	-0.14	0.88		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPFF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
951	1c11		293	345	3.8e-05	-0.02	0.22		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
951	1eh2		278	369	1.1e-31	0.58	1.00		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPFF BINDING, EF-HAND, EH 2 DOMAIN
951	1eh2		3	97	6.8e-11	0.72	0.99		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPFF BINDING, EF-HAND, EH 2 DOMAIN
951	1rr0		280	348	1.3e-05	0.33	0.98		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	
951	1rrc	A	284	345	1.5e-05	-0.21	0.23		CALCIUM BINDING PROTEIN CALMODULIN (TR-2=CS) FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	
951	1vrk	A	293	345	3.8e-05	-0.39	0.15		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
951	2pvh	A	293	348	3.8e-05	-0.13	0.25		PARVALBUMIN; CHAIN: A;	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN
951	2sep	A	283	345	5.7e-06	-0.13	0.47		BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	
952	1a75	A	310	389	0.00095	-0.81	0.05		PARVALBUMIN; CHAIN: A, B	CALCIUM BINDING PROTEIN CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
952	1aj4		280	377	5.7e-05	0.02	0.17		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
952	1au1	B	280	377	0.00038	-0.03	0.13		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
952	1br1	B	282	377	0.0019	-0.05	0.18		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
952	1bu3		310	389	0.0038	-0.24	0.05		CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM BINDING CALCIUM BINDING
952	1c07	A	279	369	5.7e-21	0.77	1.00		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
952	1c07	A	4	99	5.1e-12	0.10	0.90		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
952	1cll		293	345	3.8e-05	-0.02	0.22		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
952	1dtl	A	280	389	0.0038	-0.16	0.18		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
952	1eh2		278	369	1.1e-31	0.58	1.00		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
952	1eh2		3	97	1.7e-13	0.81	0.99		EPS15; CHAIN: NULL;	RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
952	1qjt	A	14	97	1.7e-08	0.64	0.80		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
952	1tro		280	348	1.3e-05	0.33	0.98		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	
952	1trc	A	284	345	1.5e-05	-0.21	0.23		CALCIUM BINDING PROTEIN CALMODULIN (TR=2=CS) FRAGMENT COMPRISING RESIDUES 78 - 148 (TRC 3 OF THE INTACT MOLECULE) ITRC 4	
952	1vrk	A	280	377	0.00038	-0.23	0.49		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
952	1vrk	A	293	345	3.8e-05	-0.39	0.15		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
952	2pvb	A	293	348	3.8e-05	-0.13	0.25		PARVALBUMIN; CHAIN: A;	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN
952	2scp	A	283	345	5.7e-06	-0.13	0.47		BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
953	1a09	A	319	413	3.8e-17	0.34	0.98		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU- $\alpha$ ,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
953	1a81	A	255	413	1.5e-18	0.27	0.72		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, I, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM
953	1ab2		319	417	3.8e-17	0.02	0.63		TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
953	1aot	F	319	413	1.7e-17	0.46	0.99		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOG 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
953	1aya	A	317	412	7.6e-18	0.18	1.00		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTPID, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4 PDGFR-1009 1AYA 5	
953	1bf		319	418	3.8e-19	0.36	0.82		P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
953	1csy	A	319	416	3.8e-19	0.33	0.82		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL-THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN COMPLEX
953	1cun	A	140	228	0.00013	0.05	0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	(PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)
953	1d1z	B	320	413	5.7e-18	0.04	0.49		SAP SH2 DOMAIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
953	1d4t	A	319	413	1.9e-19	0.22	0.75		T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE; CHAIN: B;	GENE REGULATION SH2 DOMAINS
953	1ffs		312	425	0.0017		58.62		GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION
953	2pld	A	319	417	9.5e-19	0.32	0.49		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C-TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029: ASP-ASN-ASP-PYR-ILE-ILE-2PLD 6	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PRO-LEU-PRO-ASP-PRO-LYS (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7	
954	1a09	A	346	440	3.8e-17	0.34	0.98		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N-N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
954	1a81	A	282	440	1.5e-18	0.27	0.72		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM
954	1ab2		346	444	3.8e-17	0.02	0.63		TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
954	1aot	F	346	440	1.7e-17	0.46	0.99		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOG 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
954	1aya	A	344	439	7.6e-18	0.18	1.00		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTP1D, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4	

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
954	1bff		346	445	3.8e-19	0.36	0.82		PDGFR-1009 1A YA 5 P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN COMPLEX
954	1csy	A	346	443	3.8e-19	0.33	0.82		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	(PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE) GENE REGULATION SH2 DOMAINS
954	1dlz	B	347	440	5.7e-18	0.04	0.49		SAP SH2 DOMAIN; CHAIN: A, B, C, D;	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION
954	1d4t	A	346	440	1.9e-19	0.22	0.75		T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCTIC ACTIVATION MOLECULE; CHAIN: B;	
954	2pld	A	346	444	9.5e-19	0.32	0.49		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C- TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029: ASP- ASN-ASP-PYR-ILE-ILE- 2PLD 6 PRO-LEU-PRO-ASP-PRO-LYS) (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
955	1al2	A	35	427	1.7e-77			150.38	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
955	1al2	A	51	423	1.7e-77	0.69	1.00		REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
957	1azw	A	85	183	0.0076	-0.16	0.05		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
957	1cvl		166	204	0.00038	-0.67	0.49		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL-HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
957	1ei9	A	86	204	7.6e-05	0.14	0.57		PALMITOYL PROTEIN THIOESTERASE I; CHAIN: A;	HYDROLASE ALPHA/BETA HYDROLASE, GLYCOPROTEIN
957	4lip	D	165	204	0.0048	-0.60	0.23		TRIACYLGLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
962	1ayz	A	2	121	3.8e-38	0.57	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
962	1ayz	A	2	121	3.8e-38			124.83	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME
962	1ayz	A	2	121	5.1e-37	0.63	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
962	1qcq	A	1	119	3.4e-40	0.62	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
962	1qcq	A	3	120	3.4e-40			70.02	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
962	2aak		1	119	3.4e-37	0.59	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
962	2aak		1	120	3.4e-37			141.95	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.5e-46	1.15	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.9e-48	0.91	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.9e-48			162.79	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1qcq	A	1	134	1.5e-50	0.63	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
963	1qcq	A	3	135	1.5e-50			102.58	UBIQUITIN CONJUGATING	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
963	2aak		1	134	3.4e-48	0.88	1.00		ENZYME; CHAIN: A; UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	CONJUGATING ENZYME, YEAST UBIQUITIN CONJUGATION UBC1;
963	2aak		1	135	3.4e-48			179.88	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE UBIQUITIN CONJUGATION UBC1;
971	1bg2		6	371	0			207.35	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
971	1bg2		7	371	0	0.39	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
971	1cz7	A	5	372	1.7e-81	0.33	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1cz7	A	7	372	1.7e-98			139.50	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1cz7	A	9	372	1.7e-98	0.34	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1dn1	B	647	825	1.3e-15	0.15	-0.18		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
971	1erj	A	1269	1643	1.7e-78	0.54	0.98		TRANSCRIPTIONAL	TRANSCRIPTION INHIBITOR BETA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									REPRESSOR TUPI; CHAIN: A, B, C;	PROPELLER
971	1got	B	1229	1600	1e-98			115.67	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	1got	B	1317	1640	1e-98	0.88	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	1got	B	1429	1660	3.4e-46	0.42	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	2kin	A	3	260	1.5e-71			135.00	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2kin	A	7	281	1.5e-71	0.09	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2kin	B	296	380	1.7e-36	-0.48	0.99		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2ncd	A	5	370	1e-81	0.34	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
971	2nod	A	7	371	1e-81			132.55	KINESIN MOTOR NCD; CHAIN: A;	NCD, CONTRACTILE PROTEIN CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
971	3kar		8	370	1.9e-91			165.99	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kar		8	370	1e-83	0.30	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kar		9	370	1.9e-91	0.19	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kin	B	298	380	3.8e-35	-0.23	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	3kin	B	298	405	6.8e-28	-0.39	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
975	1buo	A	5	125	1.7e-20	0.20	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
975	1buo	A	5	128	3.8e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	LEUKEMIA, GENE REGULATION GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
975	1buo	A	5	130	3.8e-28			58.76	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
975	1gof	•	251	464	0.0022	0.10	0.19		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
975	1gof		288	385	5.1e-10	0.03	-0.02		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
977	1bg2		1	352	6.8e-81			220.57	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
977	1bg2		2	352	6.8e-81	0.74	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
977	1cz7	A	3	352	8.5e-69			160.51	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
977	1cz7	A	5	354	8.5e-69	0.58	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
977	1dn1	B	365	430	5.7e-05	0.21	0.16		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
977	1fio	A	582	766	0.0057	-0.00	0.10		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
977	2kin	A	1	259	5.2e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	1	259	5.7e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	2	258	1.2e-55	0.38	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	2	259	5.7e-72	0.45	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	B	272	366	1.7e-17	-0.24	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	B	274	364	1.9e-36	-0.22	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2ncd	A	3	352	1.2e-68			157.70	KINESIN MOTOR NCD; CHAIN: A;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2ncd	A	5	346	1.2e-68	0.64	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
977	3kar		4	351	3.4e-66			185.54	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
977	3kar		5	348	3.4e-66	0.58	1.00			MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
977	3kin	B	276	364	1.5e-34	-0.10	0.99		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
977	3kin	B	276	366	1e-16	-0.19	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
982	1aut	L	597	670	1.5e-10	0.03	-0.19		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
982	1aut	L	745	823	1.1e-24	0.36	0.41		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
982	1eej	A	740	820	1.9e-20	-0.11	0.16		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
									MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
982	1ckl	A	3	107	1.9e-16	0.22	0.17		CD46; CHAIN: A, B, C, D, E, F;	PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
982	1d4v	A	556	658	5.7e-09	0.29	-0.12		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
982	1dan	L	738	823	6.8e-16	0.13	0.11		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
982	1dan	L	741	831	1.1e-24	-0.19	0.27		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COFACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dan	L	759	846	3.8e-24	-0.16	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COFACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dva	L	734	831	3.8e-23	-0.18	0.00		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN; CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	
982	1dva	L	738	823	6.8e-16	-0.02	0.13		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
982	1e5g	A	3	96	3.8e-17	0.18	0.33		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
982	1emn		257	337	1.7e-11	0.09	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
982	1emn		738	809	3.4e-15	-0.22	0.06		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
982	1ext	A	533	672	1.9e-10	0.07	0.01		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
982	1f7e	A	741	781	5.7e-17	0.15	0.75		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
982	1hfh		2	96	9.5e-16	0.03	0.23		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	DOMAIN, BLOOD 2 CLOTTING
982	1pfx	L	741	840	1.3e-32	-0.03	0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
982	1qfk	L	741	830	3.8e-29	0.01	0.05		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
982	1vvc		2	96	1.7e-14	0.18	-0.09		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
982	1whe		744	814	1.1e-19	-0.30	0.11		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
982	1xka	L	369	441	5.1e-10	0.04	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
982	1xka	L	741	831	1.9e-27	0.05	0.06		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
982	4mt2		557	617	1.4e-09	-0.46	0.07		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2.3	
986	1a6a	B	22	202	1.4e-46			61.03	HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
986	1a6a	B	25	201	1.4e-46	-0.06	0.39		HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
986	1a6d	B	16	201	1.4e-46			57.96	HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
986	1a6d	B	45	201	1.4e-46	-0.34	0.58		HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
986	1bx2	A	22	202	8.5e-61			95.88	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	A	28	202	8.5e-61	-0.11	0.58		HLA-DR2; CHAIN: A, D; HLA-	IMMUNE SYSTEM HLA-DR2,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
		•							DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	B	20	204	1.7e-45			59.12	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	B	45	201	1.7e-45	-0.39	0.46		HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1fv1	A	29	202	3.4e-60	-0.31	0.90		MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
986	1fv1	B	29	201	1.7e-46	-0.50	0.39		MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
986	1hdm	A	20	207	3.4e-43			282.05	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN: A; CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN: B; MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	IMMUNE SYSTEM RING6, HLA-DMA; RING7, HLA-DMB; HISTOCOMPATIBILITY PROTEIN, IMMUNE SYSTEM
986	1iak	A	20	202	1e-61			106.84		HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
986	liak	A	37	202	1e-61	-0.12	1.00		MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
986	liak	B	23	201	1.5e-43			59.46	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
986	liao	B	1	201	1.2e-43			58.50	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC, I-A, OVALBUMIN PEPTIDE
986	liea	A	21	203	5.1e-59			100.86	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	liea	A	27	203	5.1e-59	-0.28	0.95		MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	liea	B	2	199	3.4e-45			53.16	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	lieb	B	1	199	3.4e-45			58.75	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	lieb	B	51	199	3.4e-45	-0.34	0.21		MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	2iad	A	20	207	3.4e-61			109.34	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
986	2iad	A	37	206	3.4e-61	0.09	1.00		MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
986	2iad	B	2	201	3.4e-44			59.80	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
987	1a4y	A	52	214	1.9e-11	-0.43	0.60		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1a9n	A	49	130	3.8e-15	-0.29	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1a9n	A	52	199	3.8e-14	0.10	0.40		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	49	145	3.8e-15	0.07	0.94		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	52	199	5.7e-14	0.05	0.35		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1c1g	A	231	493	5.1e-19	-0.72	0.03		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
987	1d0b	A	5	162	1.2e-18	0.33	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1dce	A	34	151	1.2e-14	0.27	0.66		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
987	1ds9	A	48	150	1e-14	-0.19	0.52		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
987	1ds9	A	50	155	3.8e-15	-0.08	0.55		OUTER ARM DYNEIN; CHAIN: A;	CHLAMYDOMONAS R. GELAE CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
987	1quu	A	236	491	7.6e-07			72.54	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CHLAMYDOMONAS, FLAGELLA CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
987	1yrg	A	57	210	1.9e-12	-0.14	0.13		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA IP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
991	1qf8	A	7	123	3.8e-56	0.46	1.00		CASEIN KINASE II; CHAIN: A, B;	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR PROTEIN KINASE, 2 ZN FINGER
991	1qf8	A	7	123	6.8e-51	0.46	1.00		CASEIN KINASE II; CHAIN: A, B;	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR PROTEIN KINASE, 2 ZN FINGER
993	2occ	H	73	141	8.5e-29	0.10	0.07		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q;	OXIDOREDUCTASE FERROCYTOCHROME C/OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
994	1ddq	C	1	1076	0	-0.22	0.96		DNA-DIRECTED RNA POLYMERASE; CHAIN: A, B; DNA-DIRECTED RNA POLYMERASE; CHAIN: C; DNA-DIRECTED RNA POLYMERASE; CHAIN: D; DNA-DIRECTED	TRANSCRIPTION TRANSFERASE, TRANSCRIPTION, DNA-DIRECTED RNA POLYMERASE, 3D-2 STRUCTURE

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RNA POLYMERASE; CHAIN: E;	
995	1bor		2	50	1.4e-08	-0.39	0.05		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
995	1chc		10	51	1.7e-12	0.29	0.59		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) ICHC 3 (NMR, 1 STRUCTURE) ICHC 4	
995	1chc		6	60	5.7e-12	-0.45	0.47		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) ICHC 3 (NMR, 1 STRUCTURE) ICHC 4	
995	1fbv	A	10	51	5.1e-10	-0.04	0.52		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
995	1fbv	A	9	60	3.8e-09	-0.46	0.30		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
995	1fre		98	134	3.4e-05	-0.11	0.03		NUCLEAR FACTOR XNF7; CHAIN: NULL;	ZINC-BINDING PROTEIN ZINC-BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA-TRANSITION
995	1g25	A	6	57	0.00017	-0.33	0.46		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
995	1rmd		4	100	1.1e-16	0.13	0.49		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
996	1am9	B	277	345	7.6e-09	-0.25	0.01		STEROL REGULATORY ELEMENT BINDING PROTEIN 1A; CHAIN: A, B, C, D; DNA; CHAIN: E, F, G, H;	COMPLEX (TRANSCRIPTION REGULATION/DNA) SREBP-1A; STEROL REGULATORY ELEMENT BINDING PROTEIN, 2 BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, SREBP, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA)
996	1an2	A	277	354	3.8e-15	-0.60	0.01		MAX PROTEIN; CHAIN: A, C; DNA; CHAIN: B, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
996	1hlo	A	268	343	1.9e-13	-0.26	0.10		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*T P*GP*GP*T)-3'; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
996	1hlo	B	277	343	1.9e-12	-0.32	0.19		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*T P*GP*GP*T)-3'; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
997	1byu	A	17	139	5.1e-46	-0.02	0.64		GTP-BINDING PROTEIN RAN; CHAIN: A; B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
997	1byu	B	13	139	1.2e-46	0.17	0.72		GTP-BINDING PROTEIN RAN; CHAIN: A; B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
997	1cc0	A	23	140	3.4e-47	-0.23	0.96		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
997	1cxz	A	23	140	1e-47	-0.14	0.98		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
997	1d5c	A	22	143	1.4e-49	0.14	0.84		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
997	1ds6	A	22	140	8.5e-49	-0.05	0.88		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
997	1lbr	A	20	145	1.4e-45			68.78	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
997	1mh1		17	145	5.1e-50			52.24	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
997	1mh1		22	140	5.1e-50	-0.12	0.87		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
997	1rrp	C	19	145	1.4e-45			65.13	RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
997	1zbd	A	17	144	1.7e-53			54.15	PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
997	1zbd	A	17	144	1.7e-53			54.15	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
997	1zbd	A	18	143	1.7e-53	0.17	0.78		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
997	2ngr	A	22	141	3.4e-46	-0.07	0.89		GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
997	3rab	A	17	143	5.1e-55	0.19	0.88		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
997	3rab	A	17	145	5.1e-55			64.11	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
998	1a06		1	174	1.7e-50	-0.20	0.16		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
998	1apm	E	1	175	5.1e-66	-0.21	0.53		TRANSFERASE(PHOSPHOTRANSFERASE) SC-/AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APKS) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (SI39AS) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
998	1cmk	E	1	175	5.1e-66	-0.17	0.47		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
998	1ctp	E	1	161	1.2e-60	-0.02	0.78		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
998	1f3m	C	1	160	3.4e-53	-0.02	0.51		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
998	1koa		1	169	1.2e-38	-0.02	0.37		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
998	1kob	A	1	169	1.2e-40	-0.02	0.72		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
998	1phk		1	140	3.4e-54	0.13	0.80		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE <del>140-149</del> ;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
998	1tki	A	1	149	1.7e-34	0.18	0.75		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
998	1tki	A	1	186	1.9e-34	-0.12	0.25		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1000	1b1h	A	10	283	1.7e-27	0.28	0.40		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1000	1cs6	A	29	283	3.4e-34	0.09	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1000	1cvs	C	21	199	3.4e-25	0.08	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1cvs	D	112	284	5.1e-36	0.15	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1cvs	D	21	199	1.2e-26	0.03	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1epf	A	123	282	3.4e-18	0.11	-0.13		NEURAL CELL ADHESION	CELL ADHESION NCAM; NCAM,



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1000	1epf	A	33	201	3.4e-24	0.11	-0.09		MOLECULE; CHAIN: A, B, C, D;	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	1f2q	A	117	281	1.7e-19	0.12	0.31		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	1f2q	A	28	208	3.4e-28	0.00	0.22		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1000	1f6a	A	116	281	1e-17	0.31	0.57		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1000	1f6a	A	26	207	1.4e-27	-0.04	0.12		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1000	1fcg	A	115	281	1.7e-19	0.15	-0.12		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1000	1fcg	A	26	205	5.1e-29	0.23	0.41		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1000	1fnl	A	114	281	3.4e-17	0.05	0.06		LOW AFFINITY	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
1000	1fnl	A	24	206	1.5e-24	0.07	0.58		IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A; LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1000	1koa		207	284	5.1e-12	0.35	0.33		TTNIN; CHAIN: NULL; TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1000	1nct		213	284	3.4e-13	0.47	-0.15			MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1000	1nkr		117	282	3.4e-29	0.20	0.76		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nkr		12	113	6.8e-13	-0.51	0.22		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nkr		27	216	1e-30			71.59	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nkr		28	204	1e-30	0.22	0.87		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1000	1tnm		213	284	3.4e-13	0.37	-0.18		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1yuh	H	28	236	8.5e-07			54.09	FAB FRAGMENT; CHAIN: NULL;	IMMUNOGLOBULIN ANTI-NITROPHENOL, LAMBDA LIGHT CHAIN, IMMUNOGLOBULIN
1000	2dli	A	117	282	3.4e-29	0.22	0.51		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1000	2dli	A	26	203	5.1e-29	0.23	0.74		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1000	2feb	A	115	281	5.1e-20	0.26	-0.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1000	2feb	A	26	206	3.4e-29	0.03	0.55		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1001	1d5r	A	291	344	0.0019	-0.64	0.07		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
1003	1d5r	A	209	262	0.0019	-0.64	0.07		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1004	1d5r	A	291	344	0.0019	-0.64	0.07		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
1010	1cun	A	164	396	5.7e-16	0.04	-0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1cun	A	213	429	1.5e-16	-0.08	0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1cun	A	293	505	1.7e-13	-0.12	0.23		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1dn1	B	236	470	5.7e-18	-0.32	0.01		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1010	1ecr	A	61	288	0.0013	-0.61	0.00		REPLICATION TERMINATOR PROTEIN; CHAIN: A; DNA 16MER DUPLEX REPLICATION TERMINATOR; CHAIN: B, C;	COMPLEX (DNA-BINDING PROTEIN/DNA) TUS; TER; DNA-BINDING, DNA REPLICATION, 2 COMPLEX (DNA-BINDING PROTEIN/DNA)
1010	1fio	A	133	329	3.8e-11	0.00	0.00		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1010	1fio	A	217	401	7.6e-11	0.02	-0.12		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1010	1quu	A	75	370	1.1e-22	-0.31	0.05		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
										CONTRACTILE PROTEIN
1013	1dfn	A	109	138	1.1e-12			59.97	DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1013	1dfn	A	110	138	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1013	1dfn	A	110	138	3.4e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1014	1cii		14	636	5.7e-59			148.75	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1014	1cun	A	190	394	3.8e-15	0.12	-0.09		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	218	447	1.9e-15	0.06	0.17		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	345	583	3.8e-21	0.11	0.04		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	419	634	1.9e-19	0.44	-0.02		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	50	284	1.9e-09	-0.09	0.30		ALPHA SPECTRIN; CHAIN: A;	STRUCTURAL PROTEIN TWO

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B, C;	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	525	741	5.7e-10	-0.06	0.12		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1dg3	A	55	307	0.0057	-0.16	0.17		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1014	1dnl	B	297	509	1.5e-18	0.07	-0.07		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1dnl	B	370	598	5.7e-26	-0.04	0.23		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1dnl	B	484	733	1.7e-09	0.02	0.66		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1fio	A	361	518	1.9e-11	0.01	-0.17		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1014	1fxk	C	308	422	1.9e-05	0.08	0.01		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1014	1fxk	C	391	513	3.8e-07	0.00	0.15		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1014	1fxk	C	472	578	1.9e-05	0.26	0.22		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B;	CHAPERONE ARCHAEAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1014	1fxk	C	552	635	0.00057	0.21	0.11		PREFOLDIN; CHAIN: C; PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1014	1quu	A	272	549	1.1e-24	0.15	0.07		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	321	580	1.3e-32	0.48	0.01		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	359	630	7.6e-27	0.20	0.15		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	471	746	3.8e-17	-0.05	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	81	398	3.8e-15	-0.06	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1015	1alh	A	349	429	1.2e-23	-0.31	0.62		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	378	468	1.7e-24	0.01	-0.06		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	405	498	1.7e-26	0.11	0.03		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	472	555	1e-27	-0.37	0.28		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	1alh	A	901	981	3.4e-30	0.34	0.10		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	929	1010	3.4e-30	0.10	0.87		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1bbo		505	554	1.7e-10	-0.65	0.18		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1mey	C	349	429	1.7e-41	-0.12	0.81		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
1015	1mey	C	374	468	1.7e-42	-0.01	0.72		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	404	496	1.7e-45	-0.01	0.82		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	443	527	5.1e-47	-0.25	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA



SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	471	556	3.4e-46	-0.26	0.90		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	530	612	1.5e-36	0.01	-0.14		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	698	778	6.8e-44	0.02	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	840	953	5.1e-45	0.12	-0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	901	981	3.4e-50	0.25	0.51		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	928	1010	3.4e-50	-0.07	0.88		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	500	527	3.4e-12	-0.05	0.39		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	528	556	5.1e-11	-0.71	0.24		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	839	865	1.5e-11	0.22	-0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	926	953	1e-12	-0.03	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	982	1010	8.5e-12	0.23	0.65		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1paa		985	1013	1.7e-05	-0.38	0.96		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDUES 130 - 159) 1PAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH 1PAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 1PAA 5 REPLACED BY ALA (P131A,P133A,C140A)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	1sp1		985	1010	0.00051	-0.10	0.70		(NMR, 10 STRUCTURES) IPAA 6 SPIF3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI1
1015	1sp2		349	375	0.00017	-0.77	0.27		SPIF2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI1
1015	1sp2		985	1010	1.9e-05	-0.54	0.90		SPIF2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI1
1015	1tf3	A	377	468	6.8e-17	-0.11	0.05		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf3	A	405	496	3.4e-18	0.15	0.23		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf3	A	472	551	1.7e-18	-0.17	0.03		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	1tf3	A	929	1010	1.5e-21	-0.17	0.64		TRANSCRIPTION FACTOR IIIA; CHAIN: A, 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf6	A	405	565	8.5e-34	-0.42	0.47		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1015	1tf6	A	472	593	1.7e-28	-0.65	0.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1015	1ubd	C	351	496	7.6e-17	-0.56	0.29		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	354	468	8.5e-31	-0.39	0.28		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	384	497	1.7e-31	-0.13	0.47		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	412	527	5.1e-30	-0.38	0.54		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	479	584	1e-31	-0.26	0.57		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	813	953	6.8e-28	0.04	-0.18		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	1ubd	C	848	981	3.4e-30	0.13	0.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	908	1006	3.4e-34	0.22	0.84		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	933	1086	5.1e-27	-0.56	0.81		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	2adr		349	403	6.8e-12	-0.66	0.19		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1015	2adr		503	558	8.5e-15	-0.80	0.39		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1015	2adr		901	955	3.4e-16	0.39	0.09		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION,

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1535	gi10438986	Homo sapiens	cDNA: FLJ22557 fis, clone HSI01483.	1405	100
1535	gi15214557	Mus musculus	RIKEN cDNA 2410042D21 gene	1369	86
1536	gi12274933	Homo sapiens	mRNA for alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1 (AGXT2L1 gene).	2018	100
1536	gi12836724	Mus musculus	putative	1689	83
1536	gi15859690	Homo sapiens	unnamed protein product	1189	66
1537	gi14017847	Homo sapiens	mRNA for KIAA1815 protein, partial cds.	2117	100
1537	gi12314159	Homo sapiens	Human DNA sequence from clone RP11-207C16 on chromosome 9p23-24.3. Contains the 3' end of the gene for a novel protein similar to C. elegans R06F6.8 (Sw:Q09417) (contains KIAA1432), the 3' end of the gene for a novel protein similar to predicted yeast, plant and worm proteins, ESTs, STSs and GSSs, complete sequence.	2117	100
1537	gi10439948	Homo sapiens	cDNA: FLJ23309 fis, clone HEP11618.	1725	99
1538	gi10437187	Homo sapiens	cDNA: FLJ21144 fis, clone CAS07955.	1919	99
1538	AAB95360	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17664.	1912	99
1538	gi12851810	Mus musculus	putative	1672	84
1539	gi3327036	Homo sapiens	mRNA for KIAA0611 protein, partial cds.	4702	100
1539	gi13905302	Mus musculus	Similar to ATPase, class II, type 9A	3961	98
1539	gi6434968	Mus musculus	putative E1-E2 ATPase	3942	98
1540	AAB93976	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14051.	2580	100
1540	gi10433868	Homo sapiens	cDNA FLJ12401 fis, clone MAMMA1002796.	2580	100
1540	AAM69800	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 30106.	1108	100
1541	AAB94901	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16290.	1317	99
1541	gi10432716	Homo sapiens	cDNA FLJ11457 fis, clone HEMBA1001522.	1317	99
1541	gi12853191	Mus musculus	putative	887	62
1542	AAB73507	Homo sapiens	INCY- Human transferase HTFS-14, SEQ ID NO:14.	1698	99
1542	gi16552496	Homo sapiens	cDNA FLJ32390 fis, clone SKMUS1000177, weakly similar to PROTEIN-L-ISOASPARTATE O-	1698	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			METHYLTRANSFERASE (EC 2.1.1.77).		
1542	gi11323192	Homo sapiens	Human DNA sequence from clone P5-1022E24 on chromosome 20. Contains the 3' end of the OPR1 gene encoding Opiate receptor-like 1 protein, the GPR8 gene encoding a G protein-coupled receptor, the KIAA0835 gene encoding a protein similar to the myelin transcription factor 1 (MYT1), a novel gene, 7 CpG islands, ESTs, STSs and GSSs, complete sequence.	1156	69
1543	AAB94644	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15536.	1941	100
1543	gi14625875	Homo sapiens	mRNA for putative autophagy-related cysteine endopeptidase (AUTL1 gene).	1941	100
1543	gi14042698	Homo sapiens	cDNA FLJ14867 fis, clone PLACE1002319.	1941	100
1544	gi9967204	Macaca fascicularis	hypothetical protein	2621	100
1544	AAB88351	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0076.	2616	99
1544	gi14272556	Homo sapiens	unnamed protein product	2616	99
1545	gi12005429	Homo sapiens	homeobox-containing transcription factor HOXD1 (HOXD1) mRNA, complete cds.	1726	100
1545	gi11095618	Homo sapiens	HOX D1 protein (HOXD1) gene, complete cds.	1726	100
1545	gi15680245	Homo sapiens	homeo box D1, clone MGC:23144 IMAGE:4869019, mRNA, complete cds.	1718	99
1546	AAB95366	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17677.	2511	100
1546	gi14042538	Homo sapiens	cDNA FLJ14773 fis, clone NT2RP3004566, weakly similar to ZINC FINGER PROTEIN 84.	2511	100
1546	gi10438630	Homo sapiens	cDNA: FLJ22301 fis, clone HRC04777.	2511	100
1547	gi15559628	Homo sapiens	mitochondrial ribosomal protein S5, clone MGC:20735 IMAGE:4561399, mRNA, complete cds.	2262	99
1547	gi13620881	Homo sapiens	MRPS5 mRNA for mitochondrial ribosomal protein S5, complete cds.	2262	99
1547	gi13620883	Mus musculus	mitochondrial ribosomal protein S5	1821	79
1548	gi12697911	Homo sapiens	mRNA for KIAA1683 protein, partial cds.	1772	72
1548	gi12053239	Homo sapiens	mRNA; cDNA DKFZp434O194 (from clone DKFZp434O194); complete cds.	1690	49



SEQ ID	Hit ID	Species	Description	S score	Percent identity
1548	AAU17484	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 1049.	1659	100
1549	gi10438186	Homo sapiens	cDNA: FLJ21945 fis, clone HEP04702.	3738	99
1549	gi10441956	Homo sapiens	clone PP384 unknown mRNA.	1196	99
1549	AAU22252	Homo sapiens	HUMA- Human cardiovascular system antigen polypeptide SEQ ID No 1026.	480	98
1550	gi12852481	Mus musculus	putative	1049	56
1550	AAB18966	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	922	89
1550	AAB42781	Homo sapiens	CURA- Human ORFX ORF2545 polypeptide sequence SEQ ID NO:5090.	513	100
1551	gi6330401	Homo sapiens	mRNA for KIAA1199 protein, partial cds.	2521	97
1551	AAY25793	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 12.	1919	96
1551	gi8518188	Homo sapiens	mRNA full length insert cDNA clone EUROIMAGE 2155535.	1352	95
1552	AAB94417	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15016.	1027	99
1552	gi10434835	Homo sapiens	cDNA FLJ13018 fis, clone NT2RP3000685.	1027	99
1552	gi12837567	Mus musculus	putative	972	92
1553	gi15929411	Homo sapiens	clone IMAGE:4040789, mRNA, partial cds.	1369	100
1553	AAG03490	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7571.	450	96
1553	gi12845828	Mus musculus	putative	376	68
1554	gi9988958	Homo sapiens	F-box protein FBX30 mRNA, complete cds.	1211	100
1554	gi14043744	Homo sapiens	Similar to F-box only protein 6, clone MGC:14140 IMAGE:4054414, mRNA, complete cds.	1211	100
1554	AAB42989	Homo sapiens	CURA- Human ORFX ORF2753 polypeptide sequence SEQ ID NO:5506.	675	99
1555	gi938026	Homo sapiens	Human mRNA for RanBP1 (Ran-binding protein 1), complete cds.	916	100
1555	AAB56619	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1197.	904	99
1555	gi620083	Homo sapiens	H.sapiens mRNA for RanBP1.	904	99
1556	gi13383265	Homo sapiens	mRNA for actin related protein, complete cds.	1962	100
1556	gi16550055	Homo sapiens	cDNA FLJ30784 fis, clone FEBRA2000881, moderately similar to ACTIN 6.	1950	99
1556	gi139383	Homo sapiens	clone MGC:15664	1949	99

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	19		IMAGE:3349184, mRNA, complete cds.		
1557	gi623545	Oryctolagus cuniculus	sarcoplasmic reticulum glycoprotein	2366	96
1557	gi164861	Oryctolagus cuniculus	sarcolumenin precursor	2307	97
1557	gi496325	Gallus gallus	53 kDa glycoprotein	2160	87
1558	AAB94641	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15526.	1379	98
1558	AAG64403	Homo sapiens	SHAN- Human paneth cell enhanced expression-like protein.	1379	98
1558	AAM94028	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 126.	1379	98
1559	gi8745315	Homo sapiens	putative GTP-binding protein (GTPBP2) mRNA, partial cds.	2742	99
1559	gi13561007	Homo sapiens	Human DNA sequence from clone RP11-22124 on chromosome 6 Contains the 3' part of the POLH gene for DNA directed polymerase eta and the GTPBP2 gene for GTP binding protein 2, ESTs, STSs, GSSs and a CpG island, complete sequence.	2742	99
1559	gi8745317	Mus musculus	putative GTP-binding protein	2731	99
1560	AAG02653	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6734.	425	100
1560	gi15080459	Homo sapiens	clone MGC:9017 IMAGE:3860059, mRNA, complete cds.	425	100
1560	gi2337920	Homo sapiens	Human syntaxin 7 mRNA, complete cds.	421	98
1561	AAB94468	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15128.	4375	99
1561	gi10434944	Homo sapiens	cDNA FLJ13089 fis, clone NT2RP3002108, weakly similar to DECI PROTEIN.	4375	99
1561	gi7300581	Drosophila melanogaster	CG4845 gene product	1083	31
1562	AAU12177	Homo sapiens	GETH Human PRO305 polypeptide sequence.	226	100
1562	AAV64734	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:895.	226	100
1562	AAV81487	Homo sapiens	FUJY Human cathepsin L2.	226	100
1563	gi12052726	Homo sapiens	mRNA; cDNA DKFZp761N0411 (from clone DKFZp761N0411); complete cds.	2381	99
1563	gi14250920	Homo sapiens	mRNA for SMC6 protein.	2374	99
1563	gi14250922	Mus musculus	SMC6 protein	2163	88
1564	gi149705	Homo sapiens	mRNA for WDR9 protein	524	98

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	62		(WDR9 gene), form A.		
1564	gi14970591	Mus musculus	WDR9 protein, form A	363	79
1564	AAB34487	Homo sapiens	HUMA- Human secreted protein BLAST search protein SEQ ID NO: 105.	169	52
1565	gi6808329	Homo sapiens	mRNA; cDNA DKFZp434K0410 (from clone DKFZp434K0410); partial cds.	787	100
1565	AAB93188	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12140.	528	51
1565	AAB92702	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11102.	528	51
1566	gi12803841	Homo sapiens	Similar to retinoic acid induced 12, clone MGC:3373 IMAGE:3629369, mRNA, complete cds.	1576	99
1566	AAB26793	Homo sapiens	UYFU- Human melanoma growth related factor-1 amino acid sequence.	1199	95
1566	gi13277702	Mus musculus	retinoic acid induced 12	1182	75
1567	AAB53405	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:945.	1288	93
1567	gi29587	Homo sapiens	Human mRNA for carbonic anhydrase II (EC 4.2.1.1).	1288	93
1567	gi179795	Homo sapiens	Human carbonic anhydrase II mRNA, complete cds.	1288	93
1568	gi182146	Homo sapiens	eosinophil peroxidase (EPP) gene, exon 12 and complete cds.	3757	100
1568	gi31183	Homo sapiens	Human mRNA for eosinophil peroxidase.	3549	97
1568	gi1777378	Mus musculus	eosinophil peroxidase	3376	89
1569	AAB94183	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14500.	2405	100
1569	gi10434215	Homo sapiens	cDNA FLJ12618 fis, clone NT2RM4001666, weakly similar to HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.	2405	100
1569	gi13543955	Homo sapiens	Similar to hypothetical protein FLJ12618, clone MGC:12994 IMAGE:3504996, mRNA, complete cds.	2082	94
1570	AAB93904	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13862.	2499	99
1570	gi14286214	Homo sapiens	hypothetical protein FLJ12150, clone MGC:15043 IMAGE:3634992, mRNA, complete cds.	2499	99
1570	gi10433559	Homo sapiens	cDNA FLJ12150 fis, clone MAMMA1000422.	2499	99
1571	gi7684605	Mus musculus	smoothelin B	640	54
1571	gi768460	Mus musculus	smoothelin A	640	54

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	4				
1571	gi7547258	Mus musculus	smoothelin small isoform S1	640	54
1572	AAB95033	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16784.	1174	100
1572	gi10433442	Homo sapiens	cDNA FLJ12056 fis, clone HEMBB1002050.	1174	100
1572	gi530876	Chlamydomonas reinhardtii	amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	142	26
1573	gi12857247	Mus musculus	putative	2111	92
1573	gi10727909	Drosophila melanogaster	CG6169 gene product	688	48
1573	gi2388911	Schizosaccharomyces pombe	hypothetical PSU1-like protein	585	47
1574	AAB41954	Homo sapiens	CURA- Human ORFX ORF1718 polypeptide sequence SEQ ID NO:3436.	1765	97
1574	AAB42773	Homo sapiens	CURA- Human ORFX ORF2537 polypeptide sequence SEQ ID NO:5074.	1134	93
1574	gi17512254	Homo sapiens	hypothetical protein FLJ21156, clone MGC:29459 IMAGE:5020837, mRNA, complete cds.	1089	100
1575	AAAY40090	Homo sapiens	HUMA- Peptide sequence derived from a human secreted protein.	918	98
1575	gi12854639	Mus musculus	putative	443	69
1575	gi17066107	Homo sapiens	partial TTN gene for titin.	86	25
1576	gi10438473	Homo sapiens	cDNA: FLJ22184 fis, clone HRC00983.	3291	99
1576	gi10241712	Homo sapiens	mRNA; cDNA DKFZp761K0816 (from clone DKFZp761K0816).	1238	99
1576	gi600118	Zea mays	extensin-like protein	666	33
1577	gi16549261	Homo sapiens	cDNA FLJ30107 fis, clone BNGH41000198, weakly similar to TETRACYCLINE RESISTANCE PROTEIN, CLASS E.	1453	100
1577	gi14715055	Homo sapiens	Similar to RIKEN cDNA 1110002C08 gene, clone MGC:9564 IMAGE:3872267, mRNA, complete cds.	1453	100
1577	gi12833845	Mus musculus	putative	1339	90
1578	gi10437669	Homo sapiens	cDNA: FLJ21551 fis, clone COL06266.	1925	99
1578	AAE01791	Homo sapiens	HUMA- Human gene 22 encoded secreted protein HOHDF66, SEQ ID NO:112.	1840	99
1578	AAB417	Homo sapiens	CURA- Human ORFX	1473	99